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                            GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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AB04962 Homo sapi
AC128666 Mus muscu
AC116694 Mus muscu
AE001580 Borrelia
AC00129 Borrelia
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AC104389 Homo sapi
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AP005080 Vibrio pa
AE004286 Vibrio ch
AC084770 Homo sapi
AC10339 Rattus no
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ALIGNMENTS

PAT 26-SEP-2001

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Saccharomycetales; mitosporic Saccharomycetales; Candida
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                                                                                                                                                           Roemer,T., Jiang,B., Boone,C. and Bussey,H.
Gene disruption methodologies for drug target discovery
Patent: WO 0160975-A 51 23-AUG-2001;
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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NIKKARNKLRVIASITKETWKIDSLDNIVKEVGGTLQVSENFDDMW"
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                                                                                                                                      Lalamne, J.L. and Rocher, C.

Novel candida albicans genes and proteins coded by said genes
Patent: WO 0075305-A 11 14-DEC-2000;

HOECHST MARION ROUSSEL (FR)

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AX057345.1 GI:12310086
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Saccharomycetales; mitosporic
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Novel candida albicans genes and proteins coded by Patent: WO 0075305.A. 19 14-DEC-2000; HOECHST MARION ROUSSEL (FR) Location/Qualifiers
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
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Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                        Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L. Gene disruption methodologies for drug target discovery Patent: WO 0205378-A 6062 11-JUL-2002; Elitra Pharmsceuticals, Inc. (US)
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S.cerevisiae chromosome XIV reading frame ORF YNL260c.
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271536.1 GI:1302312
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Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 1104)
Sen-Gupta, M., Gueldener, U., Beinhauer, J., Fiedler, T. and
Hegemann, J.H.
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Direct Submission
Submitted (29-ARR-1996) Data collected by MIPS on behalf of the Submitted (29-ARR-1996) Data collected by MIPS at the European yeast chromosome XIV sequencing project. MIPS at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org
Location/Qualifiers
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Length:
Matches:
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Sequence analysis of the 33 kb long region between ORC5 and SUI1
from the left arm of chromosome XIV from Saccharomyces cerevisiae
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                                                                                         446. .667
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/db_xref="taxon:4932"
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ATX1 gene; MPA43 gene; NRD1 gene; ORC5 grape; Stata gene; suil gene.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
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/gene="ATX1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         748 GGCCAGAATGAGAATATAAAGCAGAGCTTTCTAGAAGGTAAACAGTATGGTTTACAAGTG 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580 ACTTTAATGAAAGGTTTGAAAATGAATAACGATGÁTGAAAGTGTGAGGAATTTGÁGAGG 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 HisileAspGlnTyrAsn---AsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGlu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135270.1 GI:530995
metal homeostasis factor.
metal homeostasis factor.
Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomyceties;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases I to 2961)
1 inin, 5.4. and Culotta, V.C.
The ATXI gene of Saccharomyces cerevisiae encodes a small metal homeostasis factor that protects cells against reactive oxygen
                                                                                                                                                                                                                                                                                                                                                                                                          .83 AspileMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGluLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxicity
Proc. Natl. Acad. Sci. U.S.A. 92 (9), 3784-3788 (1995)
9534958
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30
40
140
8
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Matches:
Conservative:
Mismatches:
Indels:
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58.78%
35.88%
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Best Local Similarity:
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DB:
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KEYWORDS
SOURCE
ORGANISM
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YSCATX1HF
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AUTHORS
TITLE
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                                                                                                                                                                                  complement (5754. .9443)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA65484.1"
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                                                                                                                                               Hegemann, J.H.

Direct Submission
Submitted (21-MAR-1996) J.H. Hegemann, Institute of Micro & Molecular Biology Justus-Liebig-Univ. Giessen, Frankfurter Str. 107, D- 35392 Giessen, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFEVFEDVSRAIAGEIRGFVENEDIAKNKTKQNQAQSW"
                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Saccharomyces cerevisiae'
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Yeast 13 (9), 849-860 (1997)
97377992
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PLN 29-MAR-2000

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title notine nature (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program spisplied. CAUTION: It is possible that for number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.

CDS are numbered using the following system eg SPACSHI0.01c. SP (S. pombe). A (drivnosome 1), c5HIO (cosmid name), .01 (first CDS), c (complementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequence close is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequence close. It may be shorter because we only sequence overlapping sections conce, or longer, because we arrange for a small overlapp between neighbouring submissions.
                                                                                                                                                                                                                                                                                  acetyl-coenzyme a synthetase; AMP-binding, AMP-binding; cycl; cytochrome c; glutathione s-transferase; Glycosyl hydrolase; invl; invertase; LTR; pseudogene. Schizosaccharomyces pombe (fission yeast) Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and atholieke Universiteit Leuven, Faculty of Agricultural and Applied Biological Sciences, Laboratory of Gene Technology, Kardinaal Mercierlaan 92 Blok F, B-3001 Leuven, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of yeast sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="nominal overlap with SPCC417 AL035076 S.pombe chromosome III cosmid c417."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-MAR-1998) European Schizosaccharomyces genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyne, M., Rajandream, M.A., Barrell, B.G. and Volckaert, G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .25000
/organism="Schizosaccharomyces pombe"
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/product="hypothetical protein"
/protein_id="CAB41047.1"
                                                     2146 ---CTAATAACTCTTCATCGATTAGTTAAGAT 2117
                 123 LysileAspSerieuAspAsnLeuValLysGlu 133
                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2268. .2804
/gene="SPCC191.01"
/note="SPCC191.01, len:178"
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                                                                                                                                                                            Special 25000 bp S.pombe chromosome III cosmid c191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db xref="taxon:4896"
/chromosome="I"
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/gene="SPCC191.01"
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                                                                                                                                                                                                                                           AL049644
AL049644.1 GI:4678667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                             RESULT
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              DLSGHDAFSBEKKRGKIDSTTEDEIBYKKLSTVATPIKLSRBFDKESTVAARMAALRG
KEKEEEKVVSIPLIQNLKNEDIBSIKCRNNNLLDGKKLLLEAELSAVEDNQIFSSSFP
BDKKLSLOGGLSKRQOTBEBYMSKPKLPPMLSBDELTBVBPPPIVNDILE
GYSSVYYFEALMAFKNSQXYLSVDEFRKLNLNKFTAGFYGLKQLRVGETARYK
RALTHNGAPTLKWAFTDFCKYVLAPETLTSFCIYQLALSNXSCSSKTPNKFFRKYK
RALTHNGAPTLKWAFTDFCKYVLAPETLTSFCIYQLALSNXSCSSKTPNKFFRQQLN
EKEYYYDPELRMLAYDLLEDTVEYGIIVADSDPIEQWEAAIEEDRLRELKLDVHNYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mkvnlmlkkglatatasaappkikvgvllskipiikselnbl
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KHGRERSTKQEVKLSDDSTVAFSNNQKEQSKDDVNRPVIPNDRITEADRSNDWKSLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLSRTLYLLVKDKSGTWKRPNFDLSBESKPLHVHAENBLKLLSGDQIYTWSVSATPIG
VLQDERNRTABFIVKSHILAGKRDLVASKNDAFEDFAWLTKGEISEYVPKDYFNKTEF
LLADN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSTIGAVDILNOKTITSEVAASVTSKYLOSTFSKGNTSHIEDKR
FHYGSRGSENTAFTPITPREILSLKFHYGSGSMAYSRMDGSTIVWFTHOASPDKSVE
VYI PDCCGSDKLATDLSWRPTSLIJAVGSNSSEISLLLINEKSLITASKLRTLSLGSK
TKVNTCLYDPLGNMILAATKSEKIYLPDVKKDHSSVCSLNISDISQEDNDVVYSLAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGGSHIFIGFKSGYLAILKAKHGILEVCTKIKAHTGPITEIRADPWGRNFITGSIDGN
VYWMMKS.CCELIINDLMSAYTTLOVCHLGKILGICTEDEMYFYDLNSGNLLHSKS
LANYKTDPVLKFYDPKSWY HSGKNDTLSNHFVKNERALITYKKDMFDNTMIEKRRKN
NGGGNNHNKRISKNTDRIGKDPSRPNSKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 AsnileLysiysAlaArgAsniysLeuArgValijeAlaSerileThrLysGluThrTrp 122
translation="MVGPGLGINRVRRKGVYSTKKGSGDNLLLMKRQGKHDIHDRESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 GlyGlnIleGlnGlyThrLygAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThr
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
protein_id="CAA65492.1"
Ab_xref="G1:1255966"
db_xref="SWISS-PROT:P36528"
                                                                                                                                                                                                                                                                                                    protein_id="CAA65491.1"
db_xref="GI:1255965"
db_xref="SWISS-PROT:P53851"
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Matches:
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/note="ORF N0864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="NRD1"
/note="ORF N0868"
                                                                                                                                                                                                                         5141. .16409
note="ORF N0860"
                                                                                                                                                                                                                                                                                  start=1
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223.00
58.78%
35.88%
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Pred. No.:
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Query Match:
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/db_xref="SPTREMEL:09Y7Q1"
/translation="MDWEEVTKLEENEYKRGYDEGILKGIEQGYEEAFLFGLEHAYNK
/translation="MDWEEVTKLEENEYKRGYDEGILKGIEQGYEEAFLFGLEHAYNK
YLLAGBIYGRYCFWLKEENEYGHPKIKKAHRHLEQLKSLLESLPTNNELEETDAGFDSY
WNYTAKAKVVSSLLGTKILPAEKIDANDGFE"
complement (15.132. ..15821)
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/product="very hypothetical protein"
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INTCSSERPHYPFILTKVIARKKGKHWIGSPCHSAESS"
10542. 10871
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/note="spcC191.07"
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/db_xref="G1:4678674"

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IKKATSE"
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dayOGVAPAPPDGGEGYERMAPGAETELAIAELIKAUNDROGGGIFCLDOPFRAAPDNDP
GTAVELGYMAAQGEVLAGFTTDGRMYPEKVRSYRKQAWGDALKPFTKGGSGGMEDDA
GLIVISEGFLQNVMTEGFIRMSGGFVAVDFSIQBAFTAIKDLAARLNSQH"
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/gene="SPCC191.09c"
/note="SPCC191.09c, len:229,
/note="SPCC11TY:Schizosaccharomyces pombe, 059827, glutathione
s-transferase., (230 aa), fasta scores: opt: 1220, E():0,
(78.8% identity in 226 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 IleAspIleAspAsnValLeuAsnLeuGluGluGluGlnTyrGluLeuGlyPheLysGlu 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SPCC191.07"
/noce="Pfam match to entry PF00034 cytochrome_c,
Cytochrome c"
                                                                                                                                                                                                                          note="SPCC191.06, len:138, questionable ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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protein_id="CAB41054.1"
db_xref="G1:4678675"
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12558. .12962
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/note="SPCC191.08, len:134"
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2558. .12067
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                                                                                                                        9946. .10362
/gene="SPCC191.06"
9946. .10362
/gene="SPCC191.06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="SPCC191.07"
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label=SPCC191.08
                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (12088.
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132.00
50.00%
28.03%
17.10%
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Best Local Similarity:
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DB:
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SPPLAFARRKLDHVPKKFARSIGPFLLIVFLFFNLFPTFFFLPFFFDTTKRFNLAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALIYEARING TITRELIAS VSQCAGALOSMGVGMGDEVAIYMPMIPETIIAMI VALIYEARINE SPROGRAGA VSQCAGALOSMGVGMGDEVAIYMPMIPETIIAMI VALIYEARINE SVADRVAMSCEVUTITADESHGCKRIPHGVGWVARALTE CPTIKKULYPGRABETASKYDENDWHDIIPETPRACKPERAVVANDEHPLELLYTSGG TGKPKGVVHCTGGYLLGAAATCKYVPENDLHPTDRMGCAGDVGWITGHTYIVYGPLMLGA AVTUPESTRAYDGYYDAYNEVHRITOWYIATATAIRLIQARAGNEFVEYSBRSELKYUG SVGEDIAPESFMWY VSEVVGEKGANADTYMOTETGSHIVYGLGPVTPMKPGGATLEPF GIDAVIIDPLTGKIIEGNDVEKGANADTYMOTETGSHIVYGLGPVTPMKPGGATLEPF GDANNARGHDRYILPFF GDANNARGHDRYILPFF GDANNARGHDRYILLKROYFERTEKELIMAVRSTIGPFASPRKLIFSDLPKTRSGKIMRRIIRRIKAGYBATTADEKELIMAVRSTIGPFASPRKLIFSDLPKTRSGKIMRRIIRRIKAGYBATTADEKELIMAVRSTIGPFASPRKLIFSDLPKTRSGKIMRRIIRRIKAGYBATTADEKELIMAVRSTIGPFASPRKLIFSDLPKTRSGKIMRRIIRRIKAGYBATTADEKTHAVHYAHQKKP
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                                                                                                                                                                                                                                                                                                                                                                                                                 /product="acety1-coenzyme a synthetase"
/protein_id="CAB41048.1"
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                              /db_xref="SPTREMBL:094733"
/tabs_ate_ton="MOTRRESTWHIPDIDGIRGGILLPFHDRPAEMRDLAKCNDOFFR
/tabs_ate_ton="MOTRRESTWHIPDIDGIRGGILLPFHDRPAEMRDLAKCNDOFFR
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TSSATSTPKRLSISSMDPARIHLWRQPCNVVGYDMPTPGEQKEAPPSPAQEAIPESPV
                                                                                                                                                                                         complement (4041...6029)
/gene="SPCC191.02c"
/note="SPCC191.02c, len.662, SIMILARITY:Penicillium
chrysogenum., ACSA_PENCH, acetyl-coenzyme a synthetase,
(669 aa), fasta scores: opt: 2756, E():0, (61.5% identity
in 647 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(6748. .7101)
/gene="SPCC191.03c"
/note="SPCC191.03c, len:117, very questionable ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (4359. 5675)
/gene="SPCC191.02c"
/note="Pfam match to entry PF00501 AMP-binding,
AMP-binding enzyme"
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/gene="SPCC191.04c"
/note="SPCC191.04c, len:100, questionable ORF"
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protein id="CAB41049.1"
db_xref="GI:4678670"
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protein id="CAB41051.1"
db_xref="G1:4678672"
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protein id="CAB41050.1"
db_xref="G1:4678671"
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note="SPCC191.05c, len:211"
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/gene="SPCC191.02c"
          xref="GI:4678668"
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label=SPCC191.03c
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Uniter: Summission of the Agriculture of Agrobiological Sciences, Rice Genome Research Program; Kannondai Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tsasaxienias-affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

Tel:81-298-38-7441, Fax:81-298-38-7468)

On Dec 3, 2002 this sequence version replaced gi:18307752.

Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://com.ibiology.gatech.edu/GeneMark/), GlimmerM (http://rgp.dna.affrc.go.jp/RiceHWM/), SplicePredictor (http://rgp.dna.affr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37741 TIAGATGAGACACACTATCAAACGGGTTTCAAGAATGGTTATAGTGAGGGCTTGGTGTCT 37800
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 AsnSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAlaGlnIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 IleThrasn---GlyaspLysGluvalGluaspTyrGluLysAsnIleLysLysAlaArg
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                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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2 (bases 1 to 144741)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

La Submitted (15-JUL-2001) Takuji Sasaki, National Institute of Submitted (15-JUL-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@mias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7446)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contists are based on estimates that have provided by the gubmitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

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   GCTIATAACAAATTTACTGGGGGGGGGGAAATTTATGGACGCGTGTGTTTTTGGTTGAAA 12737
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                                                                                                                                                                 105692 bp DNA linear HTG 21-MAR-2002
OJ1365 DO4, *** SEQUENCING IN PROGRESS ***.
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                                                                                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                           44 GlyPheGlnArgPheLeuIleIleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSer 63
                                                                                                   GlyGlnIleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThr 43
                                                                                                                                                                                                                                                                                                                                                             64 HislleAsp---GlnTyrAsnAsnSerSerSerLeuArgAsnHisleuAsnAsnLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 AspileMetAlaGinileSerileThrAsnGlyAspLysGluValGluAsp-----Tyr
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Oryza satīva (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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Oryza sativa nipponbare(GA3) genomic DNA,
clone:0J1365_D04
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cultivar="Nipponbare"
/db.xref="taxon:39947"
/chromosome="7"
/clone="0J1365_D04"
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2 (bases 1 to 105692)
Sasaki,T., Matsumoto,T. and Yamam
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us-09-980-054a-12.rge

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predicted by GENSCAN"
join(28697. .28907,28986. .29086,29178. .29380,29774. .30188)
/gene="P0681F05.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .30188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /COCOL_STATE_I
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/ da xref="ed1:27261055"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MGSLGRRPWVGGLTAAMIFAVAVCGFCFSGASAAAAAPTFGDNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSILWNPKQIVFFVDKVPIREYRNSDKPNTFFPIMKPMYVFSSIWNADDWATRGGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTDWTKAPFTSSYRDFTADACSWGTAAASPPSCAASTGNSWWDQPPAWALDAGQREDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="wedldigiptafppfaeanagdsgaaagskdyvhyriqqrngrk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYMCSDVDAAPQRDELDFEFLGNRTGEPYIIQTNVYRSGVGGREMRHSLWFDPTADFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .33140,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (join(27163. .27332,27442. .27529))
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complement (join(27163. .27332,27442. .27529))
/gene="p0681P05.7"
/note="This category is not included in IRGSF standard.
hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .29380,29774.
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gene="P0681P05.8"
note="contains ESTs C72892(B2426), AU172540(E2426)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="putative xyloglucan endotransglycosylase"
protein id="BAC45142.1"
db_xref="GI:27261026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join(32633. .32677,32784. .32837,32929. 33226. .33262))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (join (32633. .32677,32784. .32837,32929. 33226. .33262))
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AU075848(S20385)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 D41499 (S4032), AU094265 (E3758), AU033141 (S4032) "
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Gene="P0681F05.10"
join(36723. .36827,37444. .37566)
Gene="P0681F05.10"
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join(23817. .24701,24780. .24953)
                                                                                                                                                                                                                                                                                                                                            join(23817. .24701,24780. .24953)
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                                                                              predicted by GeneMark.hmm etc." (codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="BAC45143.1"
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                                                                                                                                                                               /proteIn_id="BAC45140.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHPELILASKODGEIVDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33226. .33262))
/gene="P0681F05.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                             CDS
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NGBI Nonzedundant Protein database with BLASTP. BSTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and 'like protein. A gene without significant homology to any protein name to indicate the homology level significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction program is also classified as a "hypothetical" protein and IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. This sequence of PoGB1POS clone has an overlap with OSJNBAD007712 (DDBJ: AP004990) clone at 5' end and with OSJNBAD044CIS (DDBJ: AP004990) and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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\textstyle codo: 27261023"
\textstyle xalation="MTDAGEGTDGEEPESEERAAARDRSDDESSAAPRLASPPPELGL
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| translation="W711048"
| translation="W711048"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join (6526. .6561,6842. .6925,7110. .7217,7735. .7831,7975. .7985))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join (6526. .6561,6842. .6925,7110. .7217,7735. .7831,7975. .7985)}
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/mol type="genomic DNA"
/cultivar="Nipponbare"
/cultivar=axon:39947"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /pseudo
join(19824. .19909,20071. .20178,20294. .20405)
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complement (join(13012. .13105,13319. .13446))
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predicted by GeneMark.hmm etc."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted by FGENESH etc."
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gene="P0681F05.4"
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Submitted (11-MAR-2003) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, GRB-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, GRB-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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SPECIFIC PRECURSOR"
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IKLQTRVAEIFGKSSTGSSNTVKVKTSDNQYYEFEELVLTTPLGWLKQNLQVFHPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(889. .1168,1306. .2585))
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complement(join(889. .1168,1306. .2585))
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/
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/note="similarity to ANON-37CS PROTEIN, Drosophila
melanogaster, SWISSPROT:A37C_DROME"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contains EST gb:AI328730, BG278778"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="20H10.010"
/number-?
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/gene="20H10.010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  889. .2585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                   complement (join(38841. 39014,39099. 39252,40484. 40510))
dene="po681F05.12"
complement (join(38941. 39014,39099. 39252,40484. 40510))
/gene="po681F05.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:::|||
50294 TTAGATGAGACACTATCAAAGGGTTTCAAGAATGGTTATAGTGAGGGCTTGGTGTCT 50353
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Neurospora crassa DNA linkage group V Cosmid contig 20H10.
BX294024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
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/db_xref="d1:27261028"
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complement (join(44510. .44803,44881. .44957,45876. .45936,46437. .46555,47886. .47958,48064. .48255,48513. .48761))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAlaGlnIleSer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 GlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPheGlnArgPheLeullelle 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 GlyTyrileGlnGluLeuMetLysPheTrpLeuSer----HislleAspGlnTyrAsn 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LeuGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGlnIleGlnGlyThrLysAsp 31
                                                                                                                                                    /note="This category is not included in IRGSP standard.
hypothetical ORF
predicted by GlimmerM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50585 CTGAAATTCAGGGTTATCACAGCAAGTTTAGGTACAAAACTGGAGTATC 50633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AsnlysLeuArgValileAlaSer-IleThrLysGluThrTrpLysile 124
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein
predicted by GlimmerM etc."
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German Neurospora genome, project.
Direct Submission
                                  /gene="P0681F05.11"
38236.38406
/gene="P0681F05.11"
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Neurospora
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                           misc_feature
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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AUTHORS
TITLE
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PSILVDDLAKIGSTVANNULDEDDRAGUSTIGNYTNUDCETOVGGREGOVNARLITULEILAG

ITVPSILVAVAVGVUTVNRNENSPIEEELUSTSTAHAGSSKAPVLAMRAIDDIEPVLK

ITVPSILVAVAVGVUTVNRNENSPIEEELUSTSTAHAGSSKAPVLAMRAIDDIEPVLK

ITVEGLINVDKRYPTIANDYLGIIQEETTPEEFENALASSVANLGGGATAALRRODTES

PVVDKEFKP FKLDVARRODVVGLNFLGGDSKLAIVLAASSVALGGGATAALRRODTES

PVVDKEFKP FKLDVARRODVGLNFLGGDSKLAIVLAASSVARTAATLA

KACIILIEDDVKTLQDVQINARGRAPAMSTPQALELCSKGFVSICEMSSAKAVVKVGKD

ENGESHVRVSVRNDLLVLETCAASTOTLISLANALTPPTPSFSKEIKKYRTSVLEVFEDLF

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LFDATMSSILGDIESWYNDGALVSTANLDVPPVSSQSBSDLDIQBNYFSSEEVKNYT

LRWNSRKNLYDQSSDAQVFKSPLVICVRDVHVIMNLYDGYDWVRTREIITKAVQDVEA
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WTADYKSTQLPGVLAGVAPVRSLVNAGSGFKDLIEIPIREKKKÖGRIFRSIGKGATAF
STTGTEVYKLGAKLALGTOYALQGAEGMLAKNPPNYNHAGPSSSAGVPAGVDYEVW
DEEDFGDHTPFKAISLALDGYAGGARGAYASLSRDIAIARDAIIAYPTEVMESSS
AQGAAKAVLMQAFTILFRPAIGVSKAIGQTLLGATNALDPNHRKRIEAKYKKH"
PRLTTAIQSIGYGCLEKVYISFPKAFWLEPDAYNNNNNNSNSNKNNRTVKGFCQWLS
PSYASAINPSRWTNEIVELGSIDPSVAHPTLLFYIYGAESEYVTSKVSSLSSSSAPSS
                                                      EFDADKNGSSPRGQNEATAAAQQFLYDFFKPYYSLLPSYSPTDPNCQPSGCLATDWLH
DDLAGNGSYCNFQVGLQEGDKDILAMRHGVPEBGVWMAGBHTATFVALGTVTGAYMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /notes "similarity to sporulation protein SP072, YNL242w, Saccharonyces cerevisiae, PIR:S63208"
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QGILDRLQIRIHKVTFQLDMQVPVBPGLSTIBLVTFQLALDBVIABGVTAPGQXKDGS
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TTETESVATTAFTTSTVRASCHRQSRPRGKTLKLSRSKNHKITFELKGVNIDVVTFPP
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                                                                                                                                                                                                                                                                                                                                                                                                                             Join(9025. .9078,9111. .15074,15144. .15161)
Gene="20H10.030"
                                                                                                                   EDVARRIAEGYGRGGVAGAGAGAGAGAGAGAGEREAAV"
                                                                                                                                                                                                                                                                                                                                                                                                     1817. .5840
/note="24 bp acaacaacaaca tandem repeat"
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//product="LRNA-Arg"
//produ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similarity to putative fatty acid desaturase mld, Homo sapiens, TREMBL:HSAF2668_1
Contains Neutral zinc metallopeptidases, zinc-binding region signature [LAIMEISHNL] |
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/product="related to putative fatty acid desaturase (mld) "
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VPFTWYHMIMITIOFPDYALVFLLPDSILGKAFFCTFGIFYALRPMAIX
HYVYEKITPEARNPDNKIPVPETFSYYGPLNWVTYNVGLHNEHHDFPAIPTAGHFIX
EIASSFYEGLPOHRSWTHVLWQFIFDEBIGMRCRVKKXVGGRVVGGTVSAKQQOPON
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                                                                                                                                                                                                                                   note="24 bp catcatcatcat tandem repeat"
15667. 15694
/note="28 bp cagacagacagacaga tandem repeat"
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/gene="20H10.040"
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                                                                                                   15144. .15161
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.5075. .15143
'gene="20H10.030"
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/product="unknown protein"
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/db_xref="G1:"A430866"
/translation="MIREMLGCCKVYISEARNKTALEAIERALKPFPPAAIVNKFEDA
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TSERGGGLASVQTMALVHGEGVIEVACNLLNPSQVGGDEVQGLIERLGREEGLLVGKG
YYTDYTPDQIVERYMDLLNNS"
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Location/Qualifiers
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this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 GAAGAAGICTTGTGTCCGGTCGTGAAGACGCTCGTCATCTGGGTTTGAAACTCGGGTTC
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                                                                                                                                                                                               /mol_type="mRNA"
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/note="RAPL09-16-J24 (R09231)"
/FLC-1) as a BamHI/XhoI insert.
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/note="artifact within
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/gene="At2g20830"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1904)
Syamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Bavis,R.W., Sckin,M., Shinn,P., Southwick,A., Shinozaki,K.,
Arabidopsis Full Length cDNA Clones
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Yameda, K. Liu, S.X., Sakano, H., Pham, P.X., Banh, J., Chung, M.K.,
Yameda, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Yameda, K., Liu, S.X., Gouch, H.L., Toriumi, M., Yu, G.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Miranda, M., Narusaka, M., Nquyen, M., Palm, C.J., Sakurai, T.,
Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.,
Direct Submission

Submitted (13-WAR-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-Length CDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
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                                                                                                                                                                                                                                                                24524 GCGCTGGTCGAGCCGACACGCTAGCGAAAGAAACACGGACGAGGCAGTGAATGATTT 24583
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Arabidopsis thaliana unknown protein (At2g20830) mRNA, complete
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                                                     24404 CAAAAAGTGGAGGATAGCCTAGAAACTTAACTCTGGGTAACAACAAGCCGGAGAAAAAA
                                                                                                                                                                 24464 GAGGAGCTGCGCCTACTGCCCAACAAGGCCCGTCTAGAAAAACATGTCTCTACCCTCTTT
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Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally

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/product = "putative major intrinsic (channel) protein"
/product = "putative major intrinsic (channel) protein"
/protein id="AAM15199.1"
/do_xref="Molives | Molives |
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%STPHIFFGGSSNYQPGSYHGGPPWDAARTTTSSRDDPPSMSNASEMQAEWIEED"
7487. 8921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="model" provided bedeen sekkttvkhknindemneefkfsvrdd kroyllefnvygwekigkhdrokganvialkeladdbekgaktroylkygwekigkhdrokganvialkeladdbegopgky roklevellykdfyfreemogavokadegrepvaggmivvivisaedvegkhtnpvyhiv frkeerktrovykknkopfkmkeefsfmleeppvhekihvevefssrigillhpkvyhir hso" hso"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="predicted protein"
/product="predicted protein"
/protein id="pAM15215.1"
/protein id="
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CKKDEHLIVACNAGGRGSRACVDLINEGYDHVANMGGGYSAWVDAGFAGDKPPEDLKI
                                                                                                                                                                                                                                                                                                                                complement (join(10013. .10504,10581. .10754))
/gene="At2g21010"
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join(-7487. .751,8023. .8247,8523. .>8921)

/gene="At2g21020"

join(7487. .7651,8023. .8247,8523. .8921)

/gene="At2g21020"
product="senescence-associated protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="hypothetical protein"
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/db_xref="G1:20197683"
                                                                                                                                                                                                                                                                     complement (4388. .5541)
/gene="At2g21040"
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/rpt_family="AT_rich"
                                                                                                                                                                                                                                                Acuo6234 11-MAR-2002
Arabidopsis thaliana chromosome 2 clone F5H14 map mil48, complete
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryopara, Unitdiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; core solds; eurosida II, Brassicales; Brassicaceae, Arabidopsis.

1 (bases 1 to 129667)
Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E., Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.I., Carrers,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (19-WAR-2000) The Institute for Genomic Research, 9712
Submitted (19-WAR-2000) The Institute for Genomic Research, 9712
3 (bases 1 to 12967)
Trown, C.D. and Xaul, S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (join(<2893. .3015,3089. .3142,3253. .3323,
3412. .3485,3566. .3643,3731. .>3840))
/gene="At2g21045"
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3412. .3485,3566. .3643,3731. .3840))
/gene="At2g21045"
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                                                                                                         467 -----GGGATCAAGGATCATCAGAGTCAAATTCAGCATC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organiam="Arabidopsis thaliana"
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/cultivar="Columbia"
/db_xref="taxon:3702"
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1. 2962
/note="Overlap with BAC clone F26H11
/AC006264:63359. 93220)."
                                                  104 IleLysLysAlaArgAsnLysLeuArgValIleAlaSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
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complement(28937.384
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FEATURES
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birren, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, V., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Randos, B., Hafer, N., Hafer, N., Hafer, N., Hafer, N., Hafer, N., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Marthews, C., McCarthy, M., Maldrim, J., Mandor, L., Minova, T., Matthews, C., McCarthy, M., Maldrim, J., Mandor, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, Travers, M., Vassiliev, H., Viel, R., Viel, R., Allson, B., Topham, R., Travers, M., Vassiliev, H., Viel, R., Vallson, B., Topham, R., Travers, M., Vassiliev, H., Viel, R., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
HTG 27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 IleMetAlaGlnileSerIleThrAsnGlyAspLysGluValGluAspTyrGluLysAsn 103
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HTG; HTGS PHASEO.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                              61306 GAAGAAGGICTTGTGTCCGGTCGTGAAGACGCTCGTCATCTGGGTTTGAAACTCGGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 HislleAspGlnTyrAsnAsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61426 CGTATTGATCCTACACGCTTCTCTCTCAGCTCCATAAGCATCTCAAGTGATTTCCATGTC
                                                                                                                                                                                    26 IleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                     46 GlnArgPheLeulleileGlyTyrIleGlnGluLeuMetLysPheTrpLeuSer----
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**SEQUENCE SAMPLING.**

**SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GGGATCAAGGATGATĊTĆAĠAĠTĆAAATTCAĠĊATĆ 61569
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Homo gapiens chromosome 11, clone CTD-2063A20
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AC137683.1 GI:25707487
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AC137683/c
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9392. .19632)
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Submitted (27-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                   Contact: sequence submissions@genome.wi.mit.edu
------------- Project Information
Center project name: L28645
Center clone name: 2063_A_20
                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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129667 31 22 53 8

Length:
Matches:
Conservative:
Mismatches:

111.00 46.49% 27.19% 14.38%

Percent Similarity: Best Local Similarity:

Score:

Query Match:

Indels: Gaps: (1-129667)

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                      Lathigra, R.
S (bases 1 to 30651)
Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Lathigr. White, O., Dodson, R., Hickey, E.K., Gwinn, M., Peterson, J., White, C., Palmer, N., Haft, D., Rosa, P. and Stevenson, B. Direct Submission
Submitted (21-UN-2002) The Institute for Genomic Researc Medical Center Dr. Rockville, MD 20850, USA
Amino acid sequence update by submitter
Location/Qualifiers
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Borrelia burgdorferi B31

Borrelia burgdorferi B31

Borrelia burgdorferi B31

Dorrelia burgdorferi B31

I (bases I to 30651)

I (bases I to 40651)

Rosa, P., Lathigra, R., Sutton, G., Peterson, J., Dodson, R.J., Haft, D., Hickey, E., Gwinn, M., White, O. and Fraser, C.M.

A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease Bpirochete Borrelia burgdorferi

Mol. Microbiol. 35 (3), 490-516 (2000)
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9564 ATGAATGGATGC---ACTTATAGAAATGCAAAATGCTCTAGAAAAGTCTCAGCAATAGAAT 9508
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Borrelia burgdorferi B31 plasmid cp32-9, complete plasmid sequence.
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Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Lathigra, R., White, O., Dodson, W., Hickey, E.K., Gwinn, M., Peterson, J., White, O., Dodson, W., Haft, D., Rosa, P. and Stevenson, B.
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gap of 100 bp
contig of 722 bp in length
gap of 100 bp
contig of 733 bp in length.
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39
33
41
26
        ) bp
706 bp in length
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Matches:
Conservative:
Mismatches:
Indels:
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AE001581.1 GI:6382346
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56795:
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57617:
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                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
        55890
55990
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56796
57518
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Pred. No.:
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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MEDLINE
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REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
AE001581
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22043 AAGCAAGAAAGTTATGATTTTTTATAAAAAAAGGGAAGTTTACTGGGTTTTTATTGGAA 22102
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22103 GAACTTCTTGAAAGTCAAACAGATTTGATTAATAAGCTTTTAAAAAAATATAAAAATTA 22162
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KIMNKONSKLSALOLGGARDARYTSALECLLKRFVDRGLIIEYKNLNLTLSPTPQ
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ISNYAIFTEEPSRSYSABABKVSFEIRAINCQKTKFNNT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22163 AAAGGATATTAAAGAGATTTTATGAGAAATTTGGTGCACAGAACATATGATATAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 HislleAspGlnTyrAsnAsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 IleMetalaGlnIleSerileThrAsnGlyAspLysGluValGluAspTyrGluLysAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 LysGlu---ThrTrpLysIleAspSerLeuAspAsnLeuValLysGluValGlyGlyThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8742. .8978
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                                                                                                                                                                                                                                                                                                                                                                                                               protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GlyTyrGlnThrGlyPheGlnArg-------
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Mismatches:
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KDFYLDSPANSFYRGVKLVPKRNSIENGSTYTNPGABTBATNPAYALSDSFTINFAPEDE

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RGSNTAAIPLVDTAKWLSEITYKVTLE"
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TAASNAITALKEPGTENLFPHYKAGYFFENALEFSINFQITIATYJAKDFDANSR
MIMLYSMLSDELHNKAHKYTLPSLQPEYINKINFYIYPTSNMQTVGLINLGTKYSNHA
YSASIAFNASVKAIEILKEEYEIAARYN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identified by sequence similarity; putative" (codon start=1 (transl_table=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to GP:1663163 percent identity: 99.21; flantified by sequence similarity; putative" codon start=1
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6170. .6736
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5784. .6173
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5395. .5796
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5717. .7805
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Search completed: February 16, 2004, 15:27:47 Job time : 3247 secs

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myosh II heavy ch
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                                                                                                                                                                                                                                                                                                                                          772
1 MSDIDIDNVLNLEEEQYELG......NLVKEVGGTLQVSENPDDMW 148
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                  February 16, 2004, 14:12:22
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      OM protein - protein search, using sw model
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G97229
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Gapop 10.0 , Gapext 0.5
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3: pir3: *

4: pir4: *
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33.5.2.3.5.5
5.5.8.5.5.5.5
5.5.8.5.5.5.5
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chromosome segrega hypothetical prote hypothetical prote RAD2 endonuclease myosin heavy chain. 6-phosphofructokin hypothetical prote lysine-tRWA ligase M protein with 5'-3' spectrin alpha cha hypothetical prote outer surface prot probable transcrip hypothetical prote probable transcrip hypothetical prote	cerevisiae) #text_change 19-Apr-2002 ler, T.; Hegemann, J.H. 996	198; 18 14; Gaps	ORFLIGYIOSLMKFWLS 63 ORFTLIGQMEGLCDV 93 KKARNKLRVIASITKETW 122 :	
A49464 T19175 T24806 MAKW MAKW AH0942 B89852 B601182 A601185 A601185 A1621 A1621 S7HUA T18501 T18501 T23701	ALIGNMENTS st (Saccharomyces tein NO838 sion 03-May-1996 inhauer, J.; Fied oatabase, April 1	Score 223; DB 2; Le Pred. No. 1.4e-10; Mismatches 40;	IDIDNVLALEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLS	
100.7 100.6	YNL260C - YPpothetical yes cerevi #sequence_ Idener, U. tein Sequen S63220	A; Experimental Source: Strain SO C; Genetics: C; Genetics: A; Gross-references: SGD:S0005204 A; Map position: 14L Query Match Best Local Similarity 35.9%; Matches 47; Conservative	IDIDNVLALEEGYELG	KIDSLDNLVKE 133 :: : -LITLHRLVKD 154
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 S6323 hypothetical protein NiAlternate names: hr CiSpecies: Saccharon CiSpace: 27-Apr-1996 CiAccession: S6323 RiSen-Gupta, th, Gus Risen-Gupta, th, Gus Airecton Aire	A,Experimental source C,Genetics: C,Genetics: A,Gene: MES:YNL260c A,Cross-references: A,Map position: 14L Query Match Best Local Similar Matches 47; Con	4 1 4 4	Cy 123 F Db 145 - RESULT 2

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probable flagellar assembly protein FliH VC2131 [imported] - Vibrio cholerae (strain NI) C; Species: Vibrio cholerae (strain S) C; Species: Vibrio cholerae (c; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C; Accession: C82114 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, i
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1.610 <KUE> A;Residues: 1.610 <KUE> A;Residues: 1.610 <KUE> A;Residues: 1.610 <KUE> A;Zross-references: 1.610 <KUE> A;Experimental source: strain B31 C;Superfamily: mismatch repair protein hexB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-627 «KLE»
A;Cross-references: GB:AE001129; GB:AE000783; NID:g2688071; PIDN:AAC66579.1; PID:g268801
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Figellar hook-associated protein (flgK) homolog - Lyme disease spirochete C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C;Accession: E70122
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bomman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, M. Authors: Smith, H.O.; Venter, J.C.
A;Althe: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Reference number: A70102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 EDQSIRKRINDFWESWHDLANQPQGLAERKIILERGKSFCEGIRNRFHSLERIYIMANDE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISITNGDKEVEDYEKNIKKARNKLRVIASITKETWK------IDSLDNLVKEVGG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 QELMKFWLSHIDQYNNS----SSLRNHLNNLEDIMAQISIINGDKEVED-YEKNIKKAR 108
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7.3;
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                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                         Query Match 12.6%; Score 97.5; Di
Best Local Similarity 24.7%; Pred. No. 3.8;
Matches 37; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 NKLRVIASITKETWKIDSLDNLVKEVGGTL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 QMDIIISKIGPKKYQLESIPNICSQYENTL 533
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                                                                                                                                                                                                                                                                                                                                                                                                       407 IGNIFSDNFLEFEPPNKNEKEEIKFNYIGQI
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Best Local Similarity
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Vugt,
B.
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Alture 402, 761-768, 1999
A; Pitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUD: 20083487; PMID: 10617197
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A; Authors: Smith, H.O.; Venter, J.C.
A; Authors: Smith, H.O.; Venter, J.C.
A; Fitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
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                                                                                                                                                                                                                                                                                                                                                                                                                          EENSQHPKIKKAHRHIBQLKSILESIP-TNNELEETDAGFDSYWNKITAKAKVVSSILGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIDOYNNSSSLRNHLNNLEDIMAQISITNGDKEVEDYEKN------IKKA 107
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A;Molecule type: DNA
A;Residues: 1-4704 <STC>
A;Residues: 1-870 <STC>
A;Cross-references: GB:AE002093; NID:g4454465; PIDN:AAD20912.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 IDIDNVLNLEBEQYELGFKEGGIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLS 63
                                                                                                                                                                                                                                                                                                                   1 MDWEEVTKLEENEYKRGYDEGILKGIEQGYEEAFLFGLEHAYNKYLLAGEIYGRVCFWLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IDNVLALBEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLS-- 63
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g20830 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%; Score 116; DB 2; Length 404; 26.0%; Pred. No. 0.082;
                                                                                                                                         Length 134
                                                                                                                                                                                                58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                   Query Match
Best Local Similarity 28.0%; Pred. No. 0.0013;
Matches 37; Conservative 29; Mismatches 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.0%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K--ETWKIDSLD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KILPAEKIDAND 131
                   C;Genetics:
A;Gene: SPDB:SPCC191.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: At2g20830
A,Map position: 2
                                                                         A; Map position:
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: Oz-Nov-2001
Sequence_revision 02-Nov-2001
C;Accession: AD008
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J.; Wren, B.W.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Fitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-2325 < CUDZ>
A;Cress-references: EMBL:U00040; NID:g474197; PID:g474199; PIDN:AAA50665.1; CESP:C18H2.3
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:C18H2.3
A;Introns: 38/1; 476/3; 488/3; 734/2; 792/3; 831/1; 939/3; 1045/1; 1091/3; 1137/1; 1204/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL590842; PIDN:CAC89567.1; PID:g15978800; GSPDB:GN00175
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GRIEGRQSELASFNDVIKPFSGYITQLHTYLETYEQ--RRRDELLQLVEKVTRQVI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 IDQYNNSSSLRNHLNNLEDIMAQIS--ITNGDKEVEDYEKNIKKARNKLRVIASITKETW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 GFQRFLIIG-YIQELMKFWLSHIDQYNNSSSLRNHLNNLEDIMAQISITNGDKEVEDYEK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C18H2.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 DNVLNLEBEQYEL - GFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IDIDNVL-----NLEEEQYELGFK------EGQIQGT--KDQYLEGKEYGY-QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.8%; Score 91; DB 2; Length 239;
Best Local Similarity 26.5%; Pred. No. 4.1;
Matches 41; Conservative 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R,Du, Z. submitted to the EMBL Data Library, April 1994 A;Description: The sequence of C. elegans cosmid C18H2. A;Reference number 218370 A;Reference number 71556 A;Accession: Tisianum. translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 KID-----SLDNLVKE-----VGGTLQVSENP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 RCELALOPAQLITLVBEALAALPMVPQQLKVYLNP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.8%; Score 91; DB:
Best Local Similarity 22.3%; Pred. No. 57;
Matches 33; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1529 NIKKMEDTLRNCSMFEKTIDGPFDEMDN 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 NIKKARNKLRVIASITKE-TWKIDSLDN 129
                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-239 < KUR>
                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T15566
R; Du, Z.
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1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
Aritile: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Reference preliminary
A; Status: preliminary
A; References: CB:AE004286; GB:AE003852; NID:G9656679; PIDN:AAF95276.1; GSPDB:GN001
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
*Athchors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.Y.Title. Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A; Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary, nucleic acid sequence not shown, translation not shown A,Moleonile type: DNA A,Residues: 1-1005 <BUL>
A,Residues: 1-1005 <BUL>
A,Cross-references: GB:U67572; GB:L77117; NID:g1591958; PIDN:AAB99331.1; PID:g1591962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 QAEGYQQGFEQGKAEGFQAGHQEGQTQGYQDGVAEGQAL--IQEQVKTFMALANQFAQPL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 SLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKID----- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- MVLALTKEVVHVEVQTNPQV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Methanococcus jannaschii
.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
.Accession: A64465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 BEEQYELGFKEGOIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein MJ1322 - Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.9%; Score 92; DB 2
Best Local Similarity 22.3%; Pred. No. 4;
Matches 33; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 SLDNLVKEV-----GGTLQVSENPDDM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 DLLN-----AQV----EKQLVD----
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C; Superfamily: hypothetical protein MJ1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.74
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                         A; Gene: VC2131
A; Map position: 1
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RESULT T47237

probable flagellar assembly protein fliH [imported] - Yersinia pestis (strain CO92)

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Genetics:

97

RESULT 8

42; Conservative Local Similarity Genome: plasmid Query Match Matches ઠે g à 셤 ઠે g 吕 ઠે ઠ :: | : : | :: | :: | :: | :: | 379 TAYQDHETSRIQLKGGELDSLK---ATVNRTSSDLEALRKNISKIKKDIHEETARLQKTKN 435 LSHIDOYNNSSSLRNHINNLEDIMAQISITNGD------KEVEDYEKNIKKARN 109 3 DIDIDN-VLNLEREQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFW 61 5 DIDNVLNLEE----EQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFW 61 hypothetical protein DKFZp434A128.1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #c;Accession: T34567 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, October 1999 A;Reference number: Z21542 A;Reference number: Z21542 CjSpecies: Naegleria fourtrieri CjDate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 CjAccession: T4723. Sybmitted to the EMBL Data Library, December 1995 Albestription: Codon usage in Naegleria fowleri. A.Reference number: 2244413 E70215
hypothetical protein BBA69 - Lyme disease spirochete plasmid A/lp54
c)species: Borrelia burgdorferi (Lyme disease spirochete)
C)ate: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
C)Accession: E70215 62 LSHIDQYNNSSSLRNHLNNLEDIMAQI-----SITNGDKEVEDYEKNIKKARNKLR 21; Gaps DB 2; Length 755; Ouery Match 11.7%; Score 90.5; DB 2; Length 746; Best Local Similarity 27.7%; Pred. No. 17; Matches 41; Conservative 28; Mismatches 58; Indels 2 myosin II heavy chain [imported] - Naegleria fowleri (fragment) Indels Status: preliminary Molecule type: mRNA Residues: 1-755 <OTT-Forsas-references: EMBL:AL122120 Experimental source: adult testis; clone DKFZp434A128 A, Cross-references: EMBL:U43192; PIDN:AAB01786.1 A, Experimental source: strain LEE mp; cell type amoeba 50; A;Status: preliminary; translated from GB/EMBL/DDBJ HNEIIOTKLKEITEKTMSVEEKATNLEDMLKE 467 110 KLRVIAS----ITKETWKID----SLDNLVKE 133 11.3%; Score 87.5; DB 23.7%; Pred. No. 29; tive 39; Mismatches 113 VIASITK-ETWKIDSLDNLVKEVGGTLQ 139 259 ETEQALKGETQKKNDADNRVKQLESELQ 286 36; Conservative Query Match Best Local Similarity A; Molecule type: mRNA A; Residues: 1-746 <SHA> A;Experimental source: C;Genetics: A;Note: DKFZp434A128.1 322 62 Best Loc Matches

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phosphoglycolate phosphatase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: AH2423
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. B, 205-213, 2001
A;Pitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .cross-references: GB.AE000790; NID:g2690224; PIDN:AAC66287.1; PID:g2690286; TIGR:BBA6:
Experimental source: strain B31
RiFraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bomain, C.; Garland, S.; Pujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A,Authors: Smith, H.O.; Venter, J.C.
A,Filte: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A,Reference number: A70100; MUID:98065943; PMID:9403685
A,Accession: E70215
A,Accession: Prolliminary; nucleic acid sequence not shown, translation not shown A,Nolecule type: DNA
A,Nolecule type: DNA
A,Residues: 1-263 <KLE>
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-212 < KUNA
A; Cross-references: GB: BA00019; PIDN: BAB76643.1; PID: g17134082; GSPDB: GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
C; Genetics:
C; Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Superfamily: Borrelia burgdorferi hypothetical protein BBI38
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11.2%; Score 86.5; DB 2;
Best Local Similarity 29.5%; Pred. No. 8.2;
Matches 38; Conservative 16; Mismatches 48;
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R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
Bmbitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 propha
A;Reference number: 217583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Corse-references: EMBL:AF020713; NID:g3025478; PID:g3025510; PIDN:AAC13005.1

A;Cunst. F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter
C; Broni, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capueno, V; Carter, N.M.; Cho
A; Ehrlich, S.D.; Emmerson, P.T.; Entrain, K.D.; Errington, J; Pabret, C; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, V.; Fuma, S.; Galizzi, A.; Galler
ech, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, K.; Lapidus, A.; Lardinois,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroecter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero,
Aceuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tosato, V.; Uchiyama,
A;Authors: Voshikawa, H.; Zumaneton, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
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C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: A/1622
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
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cobable transglycosylase - Bacillus subtilis phage SPBc2
Species: Bacillus subtilis phage SPBc2
Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
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Best Local Similarity 29.8%
Matches 28; Conservative
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A;Gene: PFB0155c
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February 16, 2004, 09:07:46; Search time 2877 Seconds (without alignments) 6356.136 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	7345	AX240813 Sequence	3762	7353 Seg	4559 Plasmodiu	95628	37	1746	ACU68949 Homo sapi	2 0	ADJOERED DEFENDED	Continuation (5 of	AC117140 Rattus no	acch	Continuation (4 of	AC010284 Homo sapi							AE014820 Plasmodiu		Arosaso Danio rer						_	ACILI404 Kattus no		Ношо	بد	Zebr	2 5	7.4	Pla	100	AC135614 Pan trogl				linear PAT 17-JAN-2001					cotina, Saccharomycetes;	ì	s coded by said genes	
£	AX057345	AX240813	AX488762	AX057353	PFMAL3P7	CNS06EVQ	AF364131	PFMAL1P3	AC068949	BX248097	ALS 2 2 2 0 0	DEMAI.701 04		AF437291	AC116984 3	AC010284	AE014843	AX485584	CNS0180K	BX511081	AE014817	HSDJ655C5	AE014820	BX276094	BX005330	PONT 1 6 5 5 1	PFA929355	SCYNLZ60C	YSCATX1HF	SCCHXIVL	AC116960	AC111404	AX344564	AC011856	PFMAL1P2_1	AL954652	AE015937	AC116984 0	DEA00304	C116957	61	ALIGNMENTS			447 bp		086			Ascomycota, Saccharomycotina	,	her, C. ns genes and proteins	. LL 14-DEC-4000;
% Query re Match Length DB	100 0 447	6.86	98.9 447	4 72.6 326	4 16.0 253305	8 15.8 863	4 15.7 4865	2 15.5 67970	15.5 178193	5.4 1/4835	0 LO.1 V4464	13:0 1/002/	4 14.9 286208	8 14.7 25753	8 14.7 110000	6 14.7 27491	4 14.6 271546	5 14.5 65	5 14.5 840	14.5 214955	5 14.5 254449	8 14.5 119733	8 14.5 250029	6 14.5 58437	6 14.5 181845	14 4 157751	4 14.4 330050	2 14.4 1104	2 14.4 2961	2 14.4 33016	2 14.4 182870	14.4 2466	2 14.4 349980	4 14.3 51014	4 14.3 110000	4 14.3 152900	4 14.3 303671	B 14.3 110000	B 14.3 347050	14.2 110000	4 14.2 115866				,	Sequence 11 from Patent	AX057345.1 GI:1231008		Candida albicans Candida albicans	ukaryota; Fungi;	יפרמדפטי	Lalanne, J.L. and Rocher, Novel candida albicans g	Š
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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100.0%; Score 447; DB 6; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 447; Conservative 0; Mismatches 0; Indels
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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MYNNEHKY GEXYKNNNNNS FYMRDDTELTDI EENI SSKKKKNKFI EKEFSYNTYRNN
KNNDENDEYGEYDNYDDNMIMSNTSNIMKKKNI KKONI FKTCINFFTTY IKPTLLLKL
                                                                                                                                                                                      /note="Similarity to P. falciparum elongation factor 1-beta, (AAF27524) (276 aa), fasta scores: opt: 366, B(): 116-15, 53.2% identity in 141 aa overlap, revised: shortened exon 2, splicing confirmed in P. knowlesi; Pfam: match to PP00796 EFIBD, EF-1 guanine nucleotide exchange domain Score 61.10, E-value 7.9e-22"
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                                                                                                                                                                                                                                                                                                                                                                                       /codon start=1
/product==elongation factor 1 (EF-1); putative"
/protain_id="CAB39068.2"
/db_xref="GI:8052274"
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Pred. No. 0.045;
0; Mismatches 176; Indels
                                                                                                                               .8583)
                                                                                         oin(7801. .7928,8084. .8234,8392.
gene="Miliap7.3"
                    oin(7801, .7928,8084, .8234,8392,
gene="MAL3P7.3"
EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="GOA:097319"
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Matches 191, Conservative
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D.melanogaster kinesin-like protein 67A (TR:P91945) BLAST

Soore: 664, sum P(2) = 1.9e-67; 28# identity in 707 as

overlap; Pfam match to PF00225 kinesin (6.1e-86), Kinesin
motor domain Score 311.54 E-value 6.1e-86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/codon_start=1
/produce="kinesin, putative"
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/db_xref="SPREMBL:097277"
/db_xref="SPREMBL:097277"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKI PINMETKKKRIMNGTKDPIHKTPYDINIVGILNKEDVSNKSNDYNTNKNIEKNNY
EKKGEYNPPHNNLTDMONSILYNIINNNVENSPHSPRMKKNVAKMLLKGNLNTANFIL
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join(5497. .5577,5689. .5787,5923. .6077,6189. .6743)
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                                                                                                                                                                                                1. .253305
/organism="Plasmodium falciparum 3D7"
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/isolate="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="synonym: PFC0860w"
                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:36329"
chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="MAL3P7.1"
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gene="MAL3P7.1"
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Fox.A.N., Pitts.R.J., Robertson,H.M., Carlson,J.R. and Zwiebel,L.J. Candidate odorant receptors from the malaria vector mosquito compises gambiae and evidence of down-regulation in response to blood feeding

Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14693-14697 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF364131 4865 bp DNA linear INV 27-NOV-2001
Anopheles gambiae putative odorant receptor Or2 gene, complete cds.
AF364131
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2 (bases 1 to 4865)
Fox,A.N., Pitts,R.J., Robertson,H., Carlson,J. and Zwiebel,L.J.
5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 TAGAAGAAGAACAATATGAATTAAGATTTAAAGAAGGTCAAATACAAGGAACAAAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 AATATTTAGAAGGAAAAAGAATATGGTTATCAAACTGGATTTCAACGATTTTTAATCATTG
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
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                                                                                                                                                                                                                                                                                   cerevisiae ORF ]"
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 863;
                                                                                                                                                                                                                                                                                                                                                          others
                                                                                                                                                                                                                                                                                                                                                                                                                        15.8%; Score 70.8; DB 11; Length 42.1%; Pred. No. 0.24; ative 45; Mismatches 177; Indels
                                                                                                             organism="Zygosaccharomyces rouxii"
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Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                           395 AAGAAGTAGGTGGAACTTTACAAGTTAGTGAAAA
                                                                                                                                /mol_type="genomic DNA"
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/db_xref="texon:4956"
/clone="AROA025B09"
/clone lib="AROA0
/note="end : T7"
                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                          SM Zygosaccharomyces rouxii

Bukaryota; Fungi; Ascomycota, Saccharomycotina; Saccharomycetes;

Bukaryota; Fungi; Ascomycota, Saccharomycotina; Saccharomycetes;

Cacharomycetales; Saccharomycetaceae; Zygosaccharomyces.

Cacharomycetales; Saccharomycetaceae; Zygosaccharomyces.

Sacharomycetales, Artiguenave, P., Blandin, G.,

Genouter, J.L., Aigle, M., Boon, E., Brottler, P., Caearegola, S.,

Genoutin, M., Dujon, B., Durrens, P., Lepingle, A., Ilorente, B.,

Malpertuy, A., Neuvegilse, C., Ozier-Kalogeropoulos, O., Potier, S.,

Saurin, W., Tekala, F., Toffano, Nioche, C., Wesolowski-Louvel, M.,

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

Peast species for molecular evolution studies

L. FEBS Lett. 487 (1), 3-12 (2000)
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This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces ervazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis & Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSOGEVQ 863 bp DNA linear STS 10-JAN-2001 To end of clone AROAA025B09 of library AROAA from strain CBS 732 of Zygosaccharomyces rouxii, sequence tagged site.
AL395628
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                                                                    AGAAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCA
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Wincker, P., Artiguenave, F. and Souciet, J.
Zygosaccharomyces rouxii
FEBS Lett. 487 (1), 52-55 (2000)
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Murphy, L.,
Harris, D.,
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                                                                   DDIRPYLERYTRRGRALLSISMI,MIGAFISACFVTYPLFVPGRGLPYGVTIPGVDLAT
PTYQVYFVLQYYLTFPACCMYIPFTGFYATCTLFALVQIAALKQRLGRIGKHGGTMAS
TGHSAGVTLFAELKECLKYHTKQIIQYNPLNSLVTHLCLLEFLEFGRMLCALLFLLSIS
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LITAAAQRPWYIKVGNVYPMTLEMFQXLLNVGSYSYFTLLRRVYN"
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                                                                                                                                                                                                                               /protein_id="AAL35507.1"
| Da xref="ed1:17105033"
|/translation="WILEBCP1" [GWNVRVWLFWSYLRRPRLSRFLVGCI PVAVLNVFQ
|FLKLYSSWGDMSELIINGYFTVLYFNLVLRTSFLVINRRKFETFFEGVAAEYALLEKN
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Submitted (27-MAR-2001) Biological Sciences, Vanderbilt University,
390 24th Ave. S., Nashville, TN 37235, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 CAAACTGGATTTCAACGATTTTTAATCATTGGTTATATTTAGAATTAATGAAATTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTG
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Plasmodium falciparum 3D7
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 4865;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 70.4; DB 3; Length 4 Pred. No. 0.18; O; Mismatches 181; Indels
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                                                                                                                                                                                                                    product="putative odorant receptor Or2"
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                                                                                                                                                                                                                                                                                                                                                                  954 g
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Best Local Similarity 51.0%;
Matches 196; Conservative
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AUTHORS
 TITLE
JOURNAL
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PFMAL1P3
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Mungall, K., Bowman, S., Atkin, R., Baker, S., Barcon, A., Desoks, K., Bulliangoorph, Corton, C. Cronin, C. Cronin, C., Corton, C. Cronin, C., Corton, C., Cronin, C., Corton, C., Cronin, C., Corton, C., Cronin, C., Destron, C., Destron, C., Destron, C., Corton, C., Cronin, C., Destron, C.,
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gene

CDS

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26439. .26559
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26439. .26559
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Matches 222; Conservative
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GDIOBLPNICRNFDVPYYASKLBENIRDIBVBDSEFYSEKUSSNEHTLHGNBNDASE
KKVYNVYTHNILMSILKTFRRILILISFYILETLIVTLGGKFIDYTMRILBGQKIPV
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NHLONPDAFTNTYRKFSSQTBIDEISRDLFHFYFHLFTINLKVSLMYRJIDNNKFVEN
NSTINRIKSTKRMEMOSLMENSLPWNIYNINGSDVSSVTFFVTSCINLFNVFVKIF
MSFYFFHIKIGSNGYOLALMLSIALYSAMILEFLPELFRSTFYRDKRIDNMHTVL
KEFKLIKMFNWESFAFYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains possible signal sequence. Signal peptide predicted SignalP 2.0 HMM (Signal peptide probabilty 0.640, signal anchor probability 0.357) with cleavage site probability 0.504 between residues 27 and 28. ScanRegExp hit to PS00867, Carbamoyl-phosphate synthase subdomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"

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/db_xref="G1:6594245"

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/db_xref="SPTREMBL:Q9UONS"

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/mrktl.com.nsizeEkv.cg/Thlps.ch.com.nsizeEkv.cg/Thlps.ch.com.nsizeEkv.cg/Thlps.ch.com.nsizeEkv.cg/Thlps.ch.com.nsizeEkv.cg/Thlps.ch.com.nsizeEkv.cg/Thlps.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd.ch.cd
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LYYNDIKNYFMYRTRYNEDYNIVVDKTFLQNENITSHDDGTSHNLKHLKNVIKNKLTN
MFKYPPFYHGAYYHKNIINKQILSGLLKAVDDNTNKKICFQEHKSNSTYNYNSSHIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKEEYENIHNSSINSTMANEFFEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKANINFN
LKRNSLALIIGANGGGKASPFHSILODPNMTHGALYIENFEKKAPILYVYPQNSNLFMG
LKRNSLALIIGANGGKASPFHSILODPNMTHGALYIENFEKKAPILYVYPQNSNLFMG
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                                                                                                                                                                                                                                                                                                                                                     LOIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVYNSKKHENDLQNVLNRAK
NNNVDKIIITGCCLAEIDKSLKICETYDPGGKFLYLSAGVHPTNCYBFIDKNKHEEKE
IIAKKEYEEFIKYFKNEQVENSKMENGNKKICDGEKDMNNLNEILLEKNLDTIPGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEKDKEYLENLKAKTIKŸPNRIVCIGEIGLDPDRLYFCSKYIQIKYFFPQLKLVQMFN
LEMPLHMROKOSETFFKLVDIYZELERSKGGVIBSTDKEDIVHIIVQNYKNLYIGVNG
CSIKSLENINAVKKIPINLLLLETDAPWCGYKKTHASYEYIKOTYEKRAYTNLKKIKN
IIKCDDNTIFKERNEPYNIADIAEITYKVRRERAVPFDLFCKK"
                                                                                                                                                                                                                                                                                                                translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV"
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Similar to Schizosaccharomyces pombe ATP-binding cassette
transporter abc1 abc1 or spac9e9.12C SWALL:ABC1 SCHPO
(SWALL:Q92337) (1427 aa) fasta scores: E(): 4.2e-08,
21.46% id in 1146 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam match to entry PF00005 ABC tran, ABC transporter, score 45.00, E-value 1.7-e09; HWMSmart hit to SM0382, ATPages associated with a variety of cellular activities, ScanRegExp hit to PS00211, ABC transporters family
deoxyribonuclease ybl055c ybl055c or ybl0512 or ybl0511 SWALL:YBF5 YEAST (SWALL:P34220) (418 aa) fasta scores: [5.1 2 5e-19, 30.47% id in 397 aa" codon_starts.
                                                                                                                                                                 /codon_state_1
/product="Tate_1"
/protein_id="Cab49076.1"
/db_xref="G1:23477010"
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/protein id="CAB63558.1"
/db_xref="G1:659426"
/db_xref="G0A:0900N4"
/db_xref="GA:0900N4"
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/gene="MAL1P3.03"
/note="Putative ABC transporter
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14884. .20352
/gene="MAL1P3.03"
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5005. .5496
/gene="MAL1P3.02"
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/gene="MAL1P3.02"
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/product="28s ribosomal RNA (A-type)"
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/gene="MALIP3.04"
/product (join (31966. .32476,32675. .32775))
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Query Match
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Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu

Contact: hum-info@sequence.stanford.edu

Conter project Information

Center project Information

Center project name: 897

Center clone name: RP11-40N17

Center clone name: RP11-40N17

Center clone name: RP11-40N17

Center clone name: RP11-40N17

Center project name: 897

Center clone name: RP11-40N17

Center clone name: RP11-40N17

Center project name: RP11-40N17

Center project name: RP11-40N17

Center project name: RP11-40N17

Center project name: RP11-40N17

Consensus quality: 12% of reads

Consensus quality: 17764 bases at least Q20

Insert size: 17760 bases at least Q20

Insert size: 178033, sum-of-contigs

Consensus quality: 177760 bases; agarcse-fp

Quality coverage: 11.2x in Q20 bases; sum-of-contigs

Consists of 2 contigs. The true order of the pieces

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* this record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                          ACU68949

178193 bp DNA linear HTG 04-APR-2001
Homo sapiens chromosome 6 clone RP11-40N17, WORKING DRAFT SEQUENCE,
                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 178193)
Abola, A.P.; Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Man, Mao, J., Komp, C., Kottler, S., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Conthwick, M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished

[Dass 1 to 178193)

Abola, Paulkner, D.,

Abola, D.,

Bruno, D.,

Conn, L.,

Dela Rosa, M.,

Faulkner, D.,

Federspiel, M.,

Faulkhov, S.,

Hansen, N.,

Harman, Z.S.,

Hyman, R.,

Mao, J.,

Marthe, R.,

Morehouse, A.J.,

Oefner, P.,

Palm, C.J.,

Ramirez, D.,

Wilhelmy, J.,

Yu, S. and

Davis, R.W.

Direct Submission

Submitted (13-MAY-2000) DNA Sequencing and Technology Center,

Stanford University, 855 California Avenue, Palo Alto,

CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ Genome Center
Center: Stanford DNA Sequencing and Technology Development
361 ACTIGGAAAATIGATICATIGGATAATITIGGIGAAAGAAGAAGIAGGIGGAACTITIACAAGIT
                                                                                                                                                                                                                                                                                                                                        AC068949
AC068949.13 GI:13540721
AC068949.13 GI:13540721
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN HOMO sapiens
Homo sapiens
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                                                                                                                                              8896 датадатададатадататат 8915
                                                                                                 421 AGTGAAAACCCCGATGATAT 440
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source

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174835 bp DNA linear HTG 03-APR-2003
.1-232M8, *** SEQUENCING IN PROGRESS ***, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                            308 ATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 CTGGATTTCAACGATTTTTAATCATTGGTTATTTCAAGAATTAATGAAATTTTGGTTAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 CCCATATAGATCAATATAATAACTCTTCACTTCGGAATCATTTGAATAATTTGGAAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 ATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 174835)
Mclaren, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
zfish-helpsasnger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 3, 2003 this sequence version replaced gi:28200814.
                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                          8 ATATAGATATAGATAATGTATTAAATTTAGAAGAAGAACAATATGAATTAGGATTTAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 AAGGICAAATACAAGGAACAAAAGATCAATATITAGAAGGAAAAAGAATATGGTTATCAAA
                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                         163 others
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                                                                              /clone="RP11-40N17"
/clone lib="RPC1 human BAC library ll"
1. .9823
/note="assembly_name:Contig12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRAFT; HTGS FULLTOP
                                                                                                                                                                                                                                                                                                                    Score 69.2; DB 2;
Pred. No. 0.1;
0; Mismatches 193;
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Center code: SC
                                                                                                                                                               clone_end:r7"
9924. .178193
/note="assembly_name:Contig13
                                                                                                                                                                                                                                                           H
                                                                                                                                                                                                                               clone end:SP6"
30999 c 30594 g 59483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danio rerio clone CH211-232M8,
/organism="Homo sapie
/mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AAATTGATTCATTGGATA 385
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Danio rerIo (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                         15.5%;
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation man other of the overlapping clone, as we submit sequence sumisation colly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sww., SWISSEROT; Tr., TERMEL; WD., WORMPEP; Information of the clone and be found at the control of the clone and be found as the control of the clone being a YAC.
                                                                           94816 АТАТАСАСТАРАРАРДАРДАРДАРТАСАРАРТАСАРАТАТАТАТАТТТАРАТАРАРАТАРА 94875
                                                                                                                                                                                                                                                                                                         94876 атаатааатаасаадатттаадатададатаатаатаадттадаттаадтаатдададтда 94935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL929250
Zebrafish DNA sequence from clone CH211-137A2, complete sequence.
                     AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA 305
                                                                                                                                     306 AAATA---TTAAAAAGGCAAGAATAAATTAAGAGTGATGATAGTATAACTAAAGAAAC 362
                                                                                                                                                                                                                                                  363 TTGGAAAATTGATTCATTGGATAATTTGGTGAAAGAAGTAGGTGGAACTTTACAAGTTAG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-JAN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquirites: Zish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jan 22, 2003 this sequence version replaced gi:27803921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute
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Contact: zfish-help@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                         94936 TTACAAATAAATAAAGT 94955
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AL929250.7 GI:27848021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94636 АДТАТААТТGCAATTAATTTGAAATAAAATAAAAAGGAAAATAAAAATAAAATAAATTAATTAATTA 94695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AGAAGGTCAAATACAAGGAACAAAGATCAATATTTAGAAGGAAAAGATATGGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATTAGATTTGGA
                                                                                                    Chemistry: Dye-terminator; 100% of reads
Consensus quality: 173639 bases at least Q40
Consensus quality: 17369 bases at least Q30
Consensus quality: 174126 bases at least Q20
Insert size: 174535; sum-of-contigs
Insert size: 177115; 1.4% error; agarose-fp
Cuality coverage: 12.09x in Q20 bases; sum-of-contigs Quality
coverage: 12.10x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 174835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46372: contig of 46372 bp in length
46472: gap of 100 bp
95245: contig of 48773 bp in length
95345: gap of 100 bp
170226: contig of 74881 bp in length
170326: gap of 100 bp
174835: contig of 4509 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:00787
fragment_chaln:1"
170327 __174835
/note="assembly_fragment:00604
fragment chaln:1
clone_end:SP6
vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.4%; Score 68.8; DB 2; 48.9%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="CHORI-211"
1. .46372
/note="assembly_fragment:01305
fragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46473._.95245
/note="assembly_fragment:01589
fragment_chain:1"
                                                                                 Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actor side:right"
30596 c 31707 g 56558 t
Project Information
                                                      Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/db_xref="taxon:7955"
/clone="CH211-232M8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .174835
/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                        Center project name: zC232M8
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Matches 215; Conservative
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Ayodeji, M., Baca, E., Baden, H.,
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Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Cardenas, V., Carter, K., Cavacos, I., Cessar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C. Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dedarich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinya, K.,
Delgado, O., Denson, S., Deramo, C., Evals, C., Palls, T., Fan, G.,
Egan, A., Bscotto, M., Eugene, C., Evals, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flags, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garafa, W., Guerra, W., Guerra, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus clone CH230-9H22, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                               128 CIGGAITTCAACGAITTTTAATCAITGGTTATATTCAAGAATTAATGAAATTTTGGTTAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 CCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 ATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 AAATTGATTCATTGGATAATTTGGTGAAAGAAGTAGGTGGAACTTTACAAGTTAGTGAAA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                             8 ATATAGATATAGATATGTATTAAATTTAGAAGAAGAACAATATGAATTAGGATTTAAAG
                                                                                                                                                                                                                                                                                                                                                      68 AAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 ATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAAA
                                                                                                                                                                                         ;
7
                                                                                                                                  Score 67.6; DB 5; Length 94434;
Pred. No. 0.21;
0; Mismatches 219; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACI25567.5 GI:24817949
HTG: HTGS. PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
/clone="CH211-137A2"
/clone lib="CHORI-211"
17026 c 17319 g 31483 t
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                                                                                                                                     15.1%;
48.8%;
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                                                                                                                                                                                            Matches 211; Conservative
                                                                                                                                                               Similarity
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SOURCE
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                                                    BASE COUNT
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VERSION
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Direct Submission

Submitted (29-UVN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 170627)

33 (bases 1 to 170627)

48 At Genome Sequencing Consortium.

Direct Submission

Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:23096537.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas assembly (a 'contig-seaffold'). Within each contig-seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence ontigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence ontygs will be indicated in the feature
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladun, S.L., Hongson, A., Hollins, J. Jackson, L. Jackson, L., Johnson, B., Johnson, R., Levan, J., Lorensuhewal, M., Malloattne, M., Mahmodd, M., Malloy, K., Martinez, E., Mawhinay, B., Mapua, P., Martin, R., Martinez, E., Mantiney, S., Mincedd, M.P., McNeill, T.Z., Meenen, E., Mantiney, S., Minchen, J., Morren, J., Morren, M., Marker, G., Minja, E., Montemayor, J., Moore, S., Mindeavijevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Mantiney, S., Munidasa, M., Murphy, M., Nair, L., Naakeris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Perer, L., Patankoch, C., Plopper, F., Poindexter, A., Perez, L., Patankoch, C., Plopper, F., Poindexter, A., Perez, L., Patankoch, C., Plopper, F., Poindexter, A., Perez, L., Patankoch, C., Shareman, S., Shen, H., Shetter, M., Sakerman, S., Shen, H., Shetter, M., Sakerman, S., Shen, H., Shetter, M., Sakerman, S., Shen, H., Shetter, M., Saker, M., Sayer, M., Walker, B., Wang, J., Wang, S., Warten, A., Walse, M., Walker, R., Walker, B., Wang, J., Walght, D., Willson, R., Wu, J., Yakub, S., Yen, J., Yoon, U., Yor, Walght, D., Willson, R., Smith, D.R., Holt, R., Smith, D., R., Holt, R., Smith, D., Walser, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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2 (bases 1 to 170627)
Worley, K.C.
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Query Match
Best Local Similarity
Matches 202; Conserv
                                                                                                                                                                         Continuation (5 of 14)
                                                                          PEMAL7P1 08
PEMAL7P1 09
PEMAL7P1 10
                                                                                                                           PFMAL7P1 11
PFMAL7P1 12
                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                              PFMAL 7P1
                                                               PFMAL 7P1
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AC117140/c
LOCUS
DEFINITION
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KEYWORDS
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                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 IGGATTICAACGATTTTAATCATTGGTTAIATTCAAGAATTAATGAAATTTGGTTAIC 188
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGICAAAIACAAGGAACAAAAGAICAAIAIIITAGAAGGAAAAGAAIAIGGIIAICAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 CCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 TATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TATAGATATAGATAATGTATTAAATTTAGAAGAAGAACAATATGAATTAGGATTTAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAA 360
                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.0%; Score 67.2; DB 2; Length 170627; ilarity 49.4%; Pred. No. 0.2; Conservative 0; Mismatches 178; Indels 0:
                                                                                                                                                                                         1 109158: contig of 109158 bp in length 1159 109258: gap of unknown length 1259 110280: contig of 1022 bp in length 1381 110380: gap of unknown length 1381 111640: contig of 1160 bp in length 11640: gap of unknown length 11640: gap of unknown length 170627: contig of 58987 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4732 others
                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end_sequence:BH341988"
. 30081 c 30017 g 54086
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close end:Sp6"
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/db_xref="taxon:10116"
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/note="clone_boundary
clone_end:Sp6
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286208 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-365F7, WORKING DRAFT SEQUENCE, 9
unordered pieces.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                   Score 66.4; DB 2;
Pred. No. 0.3;
0; Mismatches 226;
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HTG; HTGS_PHASE1; HTGS_L
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BASE COUNT
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Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department Submitted (15-NOV-2002) Human Genetics, Baylor College of Medicine, One Daylor Plaza, Houston, TX 77030, USA on Nov 6, 2002 this sequence version replaced gi:23097379.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Davila, M.L., Davis, C., Davy-Carroll, D., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Pinha, M., Burbin, X., Duval, B., Eaves, K., Egan, A., Escotto, M., Budgene, C., Faran, C.A., Falls, T., Falls, T., Falls, T., Farser, C.M., Gabisi, A., Ganta, M., Garcia, A., Garcia, A., Garcia, M., Garza, M., Gubrach, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, K., Handleo, R., Hlave, P., Hawes, A., Henderson, N., Hernandez, M., Howells, S., Hlayk, S., Hune, J., Idobird, D., Jackson, A., Hollins, B., Howells, S., Hlayk, S., Hune, J., Idobird, D., Jackson, A., Hollins, B., Howells, S., Hlayk, S., Hune, J., Idobird, D., Jackson, J., Karjet, J., Lowe, M., Jang, H., Johnson, R., Johnson, M., Martin, C., Luly, W., Liu, J., Liu, W., Liu, Y., Lorensuhewa, L., Louiseged, H., Lozado, R.J., Lu, X., Mar, S., Lu, X., Mandum, B., Manhidartne, M., Martin, R., Marti
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Submitted (08-ARR-2002) Human Genome Sequencing Center, Department
Submitted (08-ARR-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 286208)
Rat Genome Sequencing Consortium.
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Center: Baylor College of Medicine
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Weinstock,G. and Gibbs,R.A.
Direct Submission
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL Project Information

Contact: hgsc-help@bcm.tmc.edu

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66 AGAAGGTCAAATACAAGGAACAAAGATCAATATTTAGAAGGAAAAAGAATATGGTTATCA 125
                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft" sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 66.4; DB 2; Length 286208; 48.6%; Pred. No. 0.23; tive 0; Mismatches 218; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                       47440: contig of 47440 bp in length
47540: gap of unknown length
230268: contig of 182728 bp in length
230368: gap of unknown length
254735: contig of 24367 bp in length
254835: gap of unknown length
275940: contig of 21105 bp in length
277252: contig of 1212 bp in length
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organism="Rattus norvegicus"
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286208: contig of 2059
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end:Sp6"
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47541. .48868
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Best Local Similarity 48.6
Matches 207; Conservative
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LAVYLMINYWRMRNYHLTSGHHVGYBTTIIYCHVLDVIWLFLYIIFYWWAV"
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transl_table=3
producE=mitochondrial ribosomal protein"
protein_id="AAMM45891"
db_xref="G1:21105286"
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note="codon recognized: GAC"
evidence=not_experimental
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/evidence=not_experimental
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/evidence=not_experimental
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protein_id="AAM34588.1"
db_xref="G1:21105285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2251. .2323 ___/
product="tRNA-Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592. .2663
product="tRNA-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="tRNA-Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="tRNA-Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="tRNA-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="tRNA-Met"
                                                                                                                                                                                                                                                                                                                                                         product="tRNA-Leu"
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gene="VAR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5489. .6661
/gene="COB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 25753)
Patersen, K.F., Langkjaer, R.B., Hvidtfeldt, J., Gartner, J.,
Palmen, W., Ussery, D.W. and Piskur, J.
Direct Submission
Direct Submission
Microbiology, Technical University of Denmark, Building 301, Lyngby DK-2800, Denmark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF437291 25753 bp DNA circular PLN 31-MAY-2002 Saccharomyces castellii strain NRRL Y-12630 mitochondrion, complete
                                                                                                                                                                                                                         186 ATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGGAATTGGAATTTGGA 245
                                                                                                                                                                                                                                                                                                                                                                                                   246 AGATATTATGGCACAAATTTCT-ATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AAAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAAACTAAAGAAACTT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 GGAAAATTGATTCATTGGATAATTTGGTGAAAGAAGGTGGAACTTTACAAGTTAGTG 424
                                                    AACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrion Saccharomyces castellii
Saccharomyces castellii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; Saccharomycetes; (bases 1 to 2575)
Petersen, R. P., Langkjaer, R. B., Hvidtfeldt, J., Gartner, J., Palmen, W., Ussery, D. W. and Piskur, J., Inheritance and organisation of the mitochondrial genome differ between two Saccharomyces yeasts
J. Mol. Biol. 318 (3), 627-636 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/transl_table=3
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1. c25753
/organism="Saccharomyces castellii"
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evidence=not_experimental
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'mol_type="genomic DNA"
'strain="NRRL Y-12630"
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:24- .297
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product="tRNA-Val"
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gene="COX3"
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AF437291.1
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AF437291
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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/product="ATP synthase subunit 8"
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db_xref="GI:21105289"
                                                                                                                                                                                                                                                                                                   0; Mismatches 172;
                                                                                                                                   13837. .14616
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/evidence=not_experimental
13837. .14616
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                                                                                                                                                                                                                                                14.7%;
Similarity 51.0%;
30; Conservative 0
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Best Local Simil
Matches 180;
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ATPWLEAIARLEFURGGLIGVALANASLDVARHDTYYVVGHFHYVLSMGAVFBELLAG
YTYWSPQILGLYYNEKLSQIQFWLIFVGANWVFLPMHFLGINGMPRRIPDYFDAFAGW
NYISSIGAVVSMISILLFVYILXDQLVMGLTNKINNKAVVFYKTPDFWESNMVFNTNT
VKSSSLEFLLTSPPAVHSFNTPAVQS"
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FWLLPMGLVCLVTSTLVESGAGTGWTVYPPLASIQAHSGPSVDLAIFALHWTSISSLL
GAINFIVTTINMRTNGWTMHKLPLFVWAILITAVLLLLTLPVLSAGVTWLLLDRNFNT
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YQVCNILDIMPINPIKLDYDNAWFIGFFDADGTITYSFKGKYPLLTISMTNKYLVDVQ
PIKDILGGYIYPDKAKNGYYKWSIQSKQDVLDFINNYVKSNPSRTTKMNRLMLSQEFY
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'translation="MLQRWLYSTNAKDIAVLYFLLALFSGMAGTAMSLIIRLELAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFFBVAGGGDDILYEHLFWFFGTTIGPLMLYMLMNIPKCWKLLKFMITWMMSTFMALL
VKMFMNMYNQODKIRYNLNYIKYYINLLMQFLFNKNYTKRSSBTTWDMLNMSKSETVN
QSGGSM%SCADLLMSTTINNKMLNKEDIKFNQMLAGLIDGDGYFGITQNKYTSCEITM
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formslation="WTPRKSHYYLMLVNSYIIDSPQPSSINYWNMGSLLGLCLVIQI
LTGIFMANHYSSNIELEFSSVEHINRDVQGGWFLRYAHANGASFFICNYIHMGKALY
YGSYRSPRVLLWTIGVIIFILIWATAPIGYCCVYGQMSHWGATVITNLFSAIPFIGKD
                                                                                                                                   TUMUMGGFAVSNPTIQRFFALHYLPPFVIAAVVIMHMMALHIGSSNPLGITGNMDR
JPMHGYPVFKDLITVFVFLIVFSLFVFFSPNTMGHPDNYIPGNPMVTPASIVPEMYLL
PPYAILRSIPDKLMGVITMFSAILVLLVLPPTDRSVVRGNSFKVLSKLFFFLFVFNFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="G1:21105288"
translation="MLQRWLYSTNAKDIAVLYFLLALFSGMAGTAMSLIIRLELAAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OOYTHGNNOLFNYLVVGHAILMIFFMMPALIGGFGNYMLPLMIGATDTAFPRINNIG
FWLLPMGLVCLVTSTLVESGAGTGWTVYPPLASIQAHSGPSVDLAIFALHMTSISSLL
GAINFIVTTLNMRTNGMTMHKLPLFVWAILITAVLLLLTLPVLSAGVTWLLLDRNFNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFFEVAGGGDPILYEHLFWFFGHPEVYILIIPGFGIISHVVSTYSKKPVFGEISMVYA
                                                                                                                                                                                                             LLGQIGAVHVEVPYILMGQISTFLYFAYFLVFIPIISTIENILFYVGSRNNTDDLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/evidence=not_experimental
/transl_table=3
/producT="I-Scell_DNA endonuclease-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(9644. .9883,10371. .11927)
/note="LAGLIDADG type group IB intron-encoded
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gene="Cox1"
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product="cytochrome c oxidase subunit I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="codon recognized: CCA"
'evidence=not_experimental
                                                                                                                                                                                                                                                                                 note="codon recognized: AUG"
evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
evidence=not_experimental
transl_table=3
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13285. .13431
'gene="ATP8"
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NAME/KEY: misc feature
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LOCATION: (28257)...(28258)
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(c) 1993 - 2004 Compugen Ltd
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US-07-779-704B-1
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Sequence 1, Application US/08916421B

Sequence 1, Application US/08916421B

Barent No. 6503729

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: jannaschii

FILE REFERENCE: PREZYS

CURRENT APPLICATION NUMBER: US/08/916,421B

CURRENT FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

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Sequence 1, Application US/08916421B
Patent No. 6503729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 GlyAspLysGluValGluAspTyrGluLysAsnIleLysLysAlaArgAsn---LysLeu 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 ArgValileAlaSerileThrLysGluThrTrpLysIleAspSerLeuAspAsnLeuVal 131
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5 AspileAspAsnValLeuAsnLeu---GluGluGluGluGlnTyrGluLeuGlyPheLysGlu 23
                                                                                                                                                   44 GlyPheGlnArgPheLeuIleIleGlyTyr-------IleGlnGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SerieuArgAsnHisleuAsnAsnLeuGluAspIleMetAlaGlnIleSerIleThrAsn
                                                                                                           24 GlyGlnIleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThr
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NAVE/KEY: misc feature
LOCATION: (98159)..(98159)
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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ATION: (84773)..(84773)
ER INPORMATION: n equals a
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OTHER INFORMATION: n equals
NAME/KEY: misc_feature
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ION: (84808)..(84808)
INFORMATION: n equals
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OTHER INFORMATION: n equals
NAME/KEY: misc_feature
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200277 AAACTITITAGAAGAAACAAAAATATIGACATIGAAAGTAITGAAAATICATIAAAAGAG
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TITLE OF INVENTION: Proteases From Gram-Positive Organisms
TITLE REFERENCE: GC394-PCT
CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER APPLICATION NUMBER: EP9719636.4
SARAIRE FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 GluValGlyGlyThrLeuGlnValSerGluAsnProAspAsp 146
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Sequence 1, Application US/09308375
Patent No. 6300117
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44.25%
24.71%
11.85%
Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                              Query Match
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OTHER INFORMATION: n equals a. t	feature 9)(98239 ON: n equa	KEY: misc feature ION: (98266)(98266) INFORMATION: n equals a,	KEY: misc featur ION: (98343)(9 INFORMATION: n	NAME/KEY: misc_feature LOCATION: (103998)(103998) OTHER INFORMATION: n equals a, t	<pre>KEY: misc_feature ION: (148948)(1 INFORMATION: n e</pre>	KEY: misc feature ION: (163385)(1 INFORMATION: n e	CEY: misc featur ION: (191989)(INFORMATION: n	KEY: misc featur ION: (191995)(INFORMATION: n	KEY: misc featur ION: (231980)(INFORMATION: n	: misc featur : (234187)(FORMATION: n	misc reatur (234220)(NRMATION: n	misc featur (234814)(ORMATION: n	Misc reacur (309398)(RMATION: n	misc_feature (309418)(309418) ORMATION: n equals a,	misc_feature (312837). (312837) RMATION: n equals a,	KEY: misc feature ION: (312993). (312993) INFORMATION: n equals a,	misc reature (319226)(319226) DRMATION: n equals a, misc feature	rion: (1559167) rion: (559167) rion in equals a,	: misc_feature : (559241)(559241) FORMATION: n equals a,	/KEY: misc feature FION: (600992)(600992) R INFORMATION: n equals a,	: misc_feature : (622708)(622708) FORMATION: n equals a,	KEY: misc featur ION: (657081)(INFORMATION: n	CEY: misc feature ION: (657 <u>2</u> 03). (6 INFORMATION: n e	: misc_feature : (674435)(6 FORMATION: n e

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44 04 04 44 C		OTHER INFORMATION: n equa NAME/KEY: misc feature LOCATION: (1602912)(160 CATION: (1602912)(160 CATION: (1603734)(160 CATION: (1603734)(1603710)(1	Alignment Scores: 4.07e+03 Sred. No.: 84.00 Score: 84.00 Percent Similarity: 42.50% Best Local Similarity: 26.67% Query Match: 10.88% DB: 4

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Sequence 716, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION OF SECORE 1998-08-13
FRIOR EMPRICATION NUMBER: US 60/064,964
PRIOR PRILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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; OREANISM:
; INDIVIDUAL ISOLATE: Mtrp4
US-08-729-955A-2
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GENERAL INFORMATION:

APPLICANT: Birnbaumer, Lutz

APPLICANT: Birnbaumer, Lutz

APPLICANT: Birnbaumer, Lutz

APPLICANT: Birnbaumer, Lutz

TITLE OF INVENTION: Method And Compounds For Controlling

TITLE OF INVENTION: Bisential for Agonist-Activated Capacitative Ca2+

TITLE OF INVENTION: Entry

TITLE OF INVENTION: Entry

TITLE OF INVENTION: Entry

TITLE OF OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Poms, Smith, Lande & Rose
                                                                                                                                                                                                                                                                                                                            PheTrpLeuSerHisIleAspGlnTyrAsnAsnSerSerSerLeuArgAsnHisLeuAsn 79
                                                                                                                                                                                                                                                                                                                                                                                                                    80 AsnLeuGluAspIleMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAsp 99
                                                                                                                                      22 LysGluGlyGlnIleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyr
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                                              7 AspAsnValLeuAsnLeuGluGluGluGluGluTyrGluLeuGlyPhe----
US-09-980-054A-12 (1-148) x US-08-916-421B-1 (1-1664976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1122767 GATATGGTCAAATATTGGGAGAGAATAAAATATAGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Poms, Smith, Lande & Rose STREET: 2029 Century Park East, Suite 3800 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,955A
FILING DATE: October 15, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025,111
FILING DATE: AUGUST 29, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 120186
TELECOMOUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEPRX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3258 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08729955A
Patent No. 5932417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                        1122800 TTT------
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MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-729-955A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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976 TATAATGAATTATTCTCTGGAGATCCAACTTGGGTAACTGAATCTATCGGTGGTGTA--- 1032
                                                                                                                          751 GCTACTAACTTCAAAGAA--------GCTGTGCAATGGTTATACTTAGCATAT 795
                                                                                                                                                                                                                                                                                                                                82 GluAspileMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGlu 101
                                                                                                                                                                                                                                                                                                                                                                                                  102 LysAsnijeLysLysAlaArgAsnLysLeuArgValIleAla---SerIleThrLysGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 ---ThṛGlyPheGlnArgPheLeuIleIleGlyTyrIleGlnGluLeuMetLysPheTrp 61
                                                                                                                                                                    27 GlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGln------ 42
                                                                                                                                                                                                                                                                                                           LeuSerHislleAspGlnTyrAsnAsnSerSerSerLeuArgAsnHisLeuAsnAsnLeu 81
                                                                                                   7 AspAsnValLeuAsnLeuGluGluGluGluTluGlnTyrGluLeuGlyPheLysGluClyGlnIle 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class I-type Lysyl-tRNA Synthetase OCR-896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1033 ---GGTATTGACGCCGTCCGATGGTAACTAAAAC 1065
                                                                US-09-980-054A-12 (1-148) x US-09-134-001C-716 (1-2271)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 LysGluValGlyGlyThrLeuGlnValSerGluAsn 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-980-054A-12 (1-148) x US-09-508-370A-11 (1-1563)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
... NAME/KEX: lysyl t-RNA synthetase
; OTHER INFORMATION: clone described in Example 3
US-09-508-370A-11
   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
Dieter Soll
APPLICANT: Michael lbba
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/508,370A
CURRENT FILING DATE: 2000-03-10
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NG: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               к:
1998_09-09
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Sequence 11, Application US/09508370A
Patent No. 6492131
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.663
81.00
36.24%
21.48%
Best Local Similarity: 23.03%
Query Match: 10.62%
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Best Local Similari
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14 GluGluGlnTyrGluLeuGlyPheLysGluGlyGlnIleGlnGlyThrLysAspGlnTyr 33

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1087 ATGCCAAGCAAAGAATCCCTTATCAGGTCGCATTCAGACATTTAAGTGTAATCAGTCAA 1146
                                                                                                                                                                                                                                                                                                                                                                1291 TCTAAATTTGATAATATGGAAATACTAGAAGAAAATAGCAAAAAAAGGAATTAATGAACTT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1351 TTGGATTTTTTAAAGAAAATTTTGAAGTTGCCACAGAACAAGACÁTTCAAAACGÁAATA 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 AsnGlyAspLysGluValGluAspTyrGluLysAsnIleLysLysAlaArgAsnLysLeu 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 jleGlnGluLeuMetLysPheTrpLeuSerHisIleAspGlnTyrAsnAsnSerSerSer 73
                        34 LeuGluGlyLysGluTyrGlyTyrGlnThrGlyPheGlnArgPheLeuIleIleGlyTyr 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 ThrlysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPheGlnArgPhe 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GlnIleSerileThr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 ValLeuAsnLeuGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGlnIleGlnGly 28
                                                                                                                                                                                                                                                                                                                           74 LeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAla-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yesquence 27, Application US/09166350A

| Sequence 27, Application US/09166350A
| Patent No. 6440663
| GENERAL INFORMATION:
| APPLICANT: Scanlan, Matthew
| APPLICANT: Chen, Yao
| APPLICANT: Chen, Yao
| APPLICANT: Old, Lloyd
| APPLICANT: Old, Lloyd
| APPLICANT: Muth, Alex
| APPLICANT: Alex
| AP
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::|||||||
|411 TATAAATTTCAAGAGAAAATAATATA 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TrpLyslleAspSerLeuAspAsnLeu 130
                                                                                                                                                                                                                                              1147 ATATTTGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.71
80.00
40.44%
25.74%
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CRGANISM: Homo sapiens
US-09-166-350-27
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Best Local Similarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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COCATION: (51001)..(525000)

THER INFORMATION: n=a or c or g or t

AME/KEY: misc_feature
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COCATION: (480001)..(495000)
THER INFORMATION: n=a or c or g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCATION: (405001)..(420000)

THER INFORMATION: n=a or c or g or
AME/KEY: misc_feature
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INFORMATION: n=a or c or g or
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OCATION: (45001)..(465000)
THER INFORMATION: n=a or c or g or
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INFORMATION: n=a or c or g or CEY: misc_feature
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OCATION: (49501)..(510000)
THER INFORMATION: n=a or c or g or
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THER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or n=a or 
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CCATION: (36001)...(375000)
THER INFORMATION: n=a or c or g
TAME/KEY: misc_feature
CCATION: (37501)...(390000)
THER INFORMATION: n=a or c or g
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THER INFORMATION: n=a or c or g
AMAF/KEY: misc_feature

COCATION: (270001)...(285000)

THER INFORMATION: n=a or c or g
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OCATION: (345001)..(360000)
THER INFORMATION: n=a or c or g
                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (210001)..(225000)
THER INFORMATION: n=a or c or
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
COCATION: (22501)...(240000)
THER INPOMATION: n=a or c or
NAME/KEY: misc_feature
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ACCATION: (285501)..(30000)
THER INFORMATION: n=a or c or
NAME/KEY: misc_feature
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THER INFORMATION: n=a or c or
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                                                                                          NAME/KEY: misc feature
LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c
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LOCATION: (195001)..(210000)
OTHER INFORMATION: n=a or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                      ||||||:::
3521 AAAATTCAAAAACAGAAACAGAAACCCTACAAGAAGAAATAACTTCATTACAGTCTTCA 3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3581 GTACAACAATATGAAGAAAA-------AACACCAAAATCAAGCAATTGCTTGTG 3628
3371 ACCATGCAAGAATTAGAGCTGGTTAAAAAGGATGCCCAACAAACCACATTGATGAATATG 3430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 ValGluAspTyrGluLysAsnIleLysLysAlaArgAsnLysLeuArgValIleAlaSer 116
                                                                49 LeuilelleGlyTyrlleGlnGluLeuMetLysPheTrpLeuSerHislleAspGlnTyr 68
                                                                                                                                                                                                            69 AsnAsnSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAlaGlnIle 88
                                                                                                                                                                                                                                                                                                                                                    -----SerileThrAsnGlyAspLysGlu 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||::: |||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 IleThrLysGlu-ThrTrpLysIleAspSerLeuAspAsnLeuVal 131
                                                                                                                 NAME/KEY: misc feature
LOCATION: (45001). (60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g or t
OCATION: (90001)..(105000)
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THER INFORMATION: n=a or c or g or
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THER INFORMATION: n=a or c or g or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocquence 1, Application US/09198452A Patent No. 6559294 GENERAL INFORMATION: APPLICANT: Griffaic T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (15001)..(30000)
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THER INFORMATION: n=a or c or g
AMAF/KEY: misc_feature
ACATION: (30001)..(45000)

THER INFORMATION: n=a or c or g
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feature
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NAME/KEY: misc_feature
LOCATION: (645001)...(66000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (640001)...(67000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (645001)...(675000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (645001)...(60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (690001)...(705000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (705001)...(720000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (735701)..(750000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc.feature
LOCATION: (750701)..(755000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc.feature
LOCATION: (755701)..(780000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc.feature
LOCATION: (755701)..(790000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc.feature
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (795001)...(810000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (810001)...(825000)
OTHER INFORMATION: n=a or c or g or t
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INFORMATION: n=a or c or g or t
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LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or
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OCATION: (720001) ..(735000)
THER INFORMATION: nis or c or g or than EAME/KEY: misc feature
OCATION: (73501) ..(750000)
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OCATION: (600001)..(615000)
THER INFORMATION: n=a or c or g or
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LOCATION: (630001)..(645000)
THER INFORMATION: n=a or c or g or
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                   NAME/KEY: misc feature
LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (55501)..(57000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g
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INFORMATION: n=a or c or g
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OCATION: (840001)..(855000)
THER INFORMATION: n=a or c or
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INFORMATION: n=a or c or
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THER INFORMATION: n=a or c or
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LOCATION: (885001)..(900000)
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LOCATION: (585001)..(600000)
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OCATION: (825001)..(84
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US-09-25-991A-6512

Sequence 6512, Application US/09252991A

Sequence 6512, Application US/09252991A

Sequence 6512, Application US/09252991A

Sequence 6512, Application US/09252991A

SEQUENCE INFORMATION: Nucleic Acid and Amino Acid Sequences Relating TO PSEUDOMONAS

TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT RELIAN DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 6512

LENGTH: 417
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                                                                                                                                                                                                                                                                                                                                                   27 GInGlyThrLysAspGlnTyr----LeuGluGlyLysGluTyrGlyTyrGlnThrGly 44
                                                                                                                                                                                                                                                                                                                                                                                                                        45 PheGlnArgPheLeulleIleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSerHis 64
                                                                                                                                                                                                                                                                              7 AspAsnValleuAsnLeuGluGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGlnIle 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200098 ------GAGTTCTTTGTTAGCTCGGGAATATCAGGGACTCATG 200136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ThrTrpLys1leAspSerLeuAspAsnLeuValLysGluValGlyGlyThrLeu 138
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229
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
OTHER INFORMATION: n=a or c or g or LOCATION: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc_feature
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6512
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80.00
39.86%
28.26%
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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APPLICAMT: WARCON Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS,
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 101196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLICATION NUMBER: US 60/094,190
PRIOR PLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6495
LENGTH: 1521
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                                                                                                                                    207 GGTTTCAACCGCGTCAGCCTCGGCGTACAGGACTTCGACATGGAGGTGCAGAAGGCGGTC 148
                                                                                                                                                                                    109 AsniysieuArgValileAlaSerIleThriysGluThrTrpLysIleAspSerLeuAsp 128
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                                                                      267 GGCATCGAGATCGACCGGCGCGAGCCGACTGGTCGACCATGGGCCTGCTCCGCGAACTC 208
                                                                                                              89 SerileThrAsnGlyAspLysGluValGluAspTyrGluLysAsnIleLysLysAlaArg 108
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                                    ---IleMetAlaGlnIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-980-054A-12 (1-148) x US-09-252-991A-6495 (1-1521)
                                                                                                                                                                                                                        147 AACCGCATGCAGACC-----CCGGAGGAGACC--
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                   120 CGTACCATCGTCGAGGCCGCGCGCCCTGCAA 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  996 CTCAGTCCCGGCCAATTGCGCGAACTCATG
                                                                                                                                                                                                                                                                                                                                                                         Sequence 6495, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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78.00
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Query Match:
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6539
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                                                                            TCCCGCGAGCAGCTGGACTGCACTTCGGT-----GGCGGAACCCCGACCTTC 131
                                                                                                                                                                                                                                           SerileThrAsnGlyAspLysGluValGluAspTyrGluLysAsnIleLysLysAlaArg 108
                                                                                                                                                                                                                                                                                                                                                                                             273 GGTTTCAACCGCGTCAGCCTCGGCGTACAGGACTTCGACATGGAGGTGCAGAAGGCGGTC 332
                                                                                                                                                                                                                                                                                                                                                                                                                               AsnLysLeuArgValIleAlaSerIleThrLysGluThrTrpLysIleAspSerLeuAsp 128
                                                                                                                              LeullelleglyTyrIleglnGluLeuMetLysPheTrpLeuSerHislleAspGlnTyr 68
                                                                                                                                                                                                                                                                               84 -----IleMetAlaGlnIle 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 ThrlysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPheGlnArgPhe 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuileileglyTyrileglngluLeuMetLysPheTrpLeuSerHisIleAspGlnTyr 68
                                                                                                                                                                                                                                                                                                         213 GGCATCGAGATCGACCGGCGAGGCCGACTGGTCGACCATGGGCCTGCTCCGCGAACTC
                                                    ThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPheGlnArgPhe
                                                                                                                                                                                                      AsnAsnSerSerLeuArgAsnHisLeuAsnAsnLeuGluAsp------
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222
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                US-09-980-054A-12 (1-148) x US-09-252-991A-6512 (1-417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 AACCGCATGCAGACC------CCGGAGGACC
                                                                                                                                                    CTCAGTCCCGGCCAATTGCGCGAACTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 CGTACCATCGTCGAGGCCGCGCGCACCTGCAA 392
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Sequence 6539, Application US/09252991A
Patent No. 6551795
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78.00
38.93%
22.14%
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Best Local Similarity;
Query Match:
DB:
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Pred. No.:
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ORGANISM: 1
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US-09-2
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94 AsplysGlu-------ValGluAspTyrGluLysAsnIleLysLysAlaArg 108
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| 11|::: :::|||
| AAAAAAGAAGAAGTAAAGGTTCGTGAAGTAGGTAAACTCTTTAGTTCAACT 678
---AATAGACTGTTACACATCAAACATGAAGAAGTTGAGAAACATAACAAACCTAAC 438
                                                     58 -------MetLygPheTrpLeuSerHiBIleAspGlnTyrAsnAsnSerSer 73
                                                                                                                                                                 74 LeuargasnHisLeuasnAsnLeuGluaspIleMetalaGlnIleSerIleThrasnGly 93
                                                                                                                                                                                                                                                                                                                                                                                            109 AsniysLeuArgValIleAlaSerIleThrLysGluThrTrpiysIleAspSer----
                                                                                            APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: LESNIEWSKI, RICHARD R
APPLICANT: STEWART, JAMES L
APPLICANT: RUPPRECHT, KEVIN R
ATITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 ------LeuAspAsnLeuValLysGlu 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   679 AAAGCTGGTCTGGATCAACAAATTCAAGAG 708
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
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APPLICATION NUMBER: US/08/179,896
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APPLICATION NUMBER: US 07/572,822
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CASEY, JAMES M
DAILEY, STEPHEN H
DAWSON, GEORGE J
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LA
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APPLICANT:
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                                      us-08-923-992A-3
; Sequence 3, Application US/08923992A
; Sequence 3, Application US/08923992A
; Patent No. 628073B
; GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 628073B-1gA FC Binding Forms of the Group B
TITLE OF INVENTION: No. 628073B-1gA FC Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
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CAMPUTER: ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bum PC compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US (08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION NUMBER: US 60/024,707
PILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Essenoid, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/POCKET NUMBER: 32,893
REFERENCE/POCKET NUMBER: 32,893
REGISTRATION NUMBER: 31,2893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 33,893
REGISTRATION
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Conservative:
Mismatches:
Indels:
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STRANDEDNESS: double
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FEATURE:
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COUNTRY: U.S.
ZIP: 60065-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
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Best Local Similarity:
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FCT-US92-06965A-14
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| CTCTABACTCCCACTACCAGGACGTTCTGAAAGAAGTTAAAGCTGCTGCTTCTAAAGTT 795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 ThrLysGluThrTrpLysIleAspSerLeuAspAsnLeuValLysGluValGlyGlyThr 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   916 ATCAACTCTGTTTGGAAA---GATCTGCTGGAAGACAACGTTACCCCGATCGACACACC 972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LeuGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGlnIjeGlnGlyThrLysAsp 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ileGlyTyrileGlnGluLeuMetLysPheTrpLeuSer-----Hisile----- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------AspGlnTyrAsnAsnSerSer 72
                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-980-054A-12 (1-148) x US-08-867-611-9 (1-1488)
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        US 07/748,566
                                                               REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834
TELEPHONE: 708-937-6365
TELEPHONE: 708-937-6566
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 SerLeuArgAsnHisLeuAsn--
APPLICATION NUMBER: US 07/748
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRIGILLA E
                                                                                                                                                                                                                         ACLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                   1.73
77.50
32.60%
20.44%
10.04%
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Query Match:
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PCT-US92-06965A-14
                                                                                                                                                                                                                                                                                      NAME/KEY:
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US-08-867-611-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGlnIleGlnGlyThrLysAsp 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ileGlyTyrIleGlnGluLeuMetLysPheTrpLeuSer-----HisIle---
Sequence 14, Application PC/TUS9206965A
GENERAL INFORMATION:
APPLICANT: DEVARE, S.
APPLICANT: DAILEY, S.
APPLICANT: JEBORATORIES
ADDRESSEE: ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                        COMPUTER KEALABLE FORM

WEDDIUM TYPE: FIDAPY disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06965A
FILING DATE: 19920821
CLASSIFICATION:
ATTONRY/AGRNT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REPRENCE/DOCKET NUMBER: 33,207
TELEPRANICATION INFORMATION:
TELEPRANICATION INFORMATION:
TELEPRAN: 708-937-6365
TELEPRAN: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-980-054A-12 (1-148) x PCT-US92-06965A-14 (1-1488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                              E: ABBOTT LABORATORIES ONE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 GlnTyrLeuGluGlyLysGlu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
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77.50
32.60%
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TCTCTAGACTCCCACTACCAGGACGTTCTGAAAGAAGTTAAAGCTGCTGCTTCTAAAGTT 795
                                                                                         796 AAAGCTÁACCTGCTGTTGAAGAAGCATGCTCTCTGÁCCCCGCCGCACTCTGCTAAA 855
                                                                                                                             98 GluAspTyrGluLysAsnIleLysLysAlaArgAsnLysLeuArgVallleAlaSerIle 117
                                                                                                                                                                856 TCTAAATTCGGTTACGGTGCTAAAGACGTTCGTTGCCACGCTCGTAAAGCTGTTACCCAC 915
                                                                                                                                                                                                  118 ThrLysGluThrTrpLysIleAspSerLeuAspAsnLeuValLysGluValGlyGlyThr 137
                                                     -----AsnLeuGluAspIleMetAlaGlnIleSerIleThrAsnGlyAspLysGluVal 97
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Robinson, John M
APPLICANT: Pilot Amatias, Tami J
APPLICANT: Hunt, Jeffrey C
TITLE OF INVENTION: Borrelia burgdorferi antigens
TITLE OF INVENTION: and uses thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/500,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Illinois
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: READABLE FORM: DC. DOS. MS-DOS.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,704
FILING DATE: 21-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08500222 Patent No. 5643733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATACHE MONE, WEAR KHING
REGISTRATION NUMBER: 33561
REGISTRATION NUMBER: 5051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-936
INFORMATION: 708-937-9556
INFORMATION SEQUENCE CHARACTERISTICS:
ERUGTH: 1497 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGI.
MOLECULE TYPE: DN
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NA ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                     :::
973 ATC 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| ::::::
736 AAGATCTCAGACCCGAGAATACTTCAAAGGCTATTAATTTTATTCAGACAACAGAGG 795
                                                                                                                                                                                  436 chcgacgengaaggaangeachdrachterereseseseaceatheerresgarestaar 495
                                                                                                                                                                                                                                                676 GCTCAGGAAGTTCCTGGCACAGGTGTGGATACCCCTGAAAATCCGTCGACAGGGCTTATG 735
                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                         --Tyr 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LeuGluGluGluGluTyrGluLeuGlyPheLysGluGlyGlnIjeGlnGlyThrLysAsp
                                                                                                                                                                                                                                                                                                                                                             51 ileGlyTyr1leGlnGluLeuMetLysPheTrpLeuSer-----HisIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 HisLeuAsnAsnLeuGluAspIle------MetAlaGlnIleSerIleThrAsnGly
1497
34
27
46
65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 -----AspGlnTyrAsnAsnSerSerLeu----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 ---IleAlaSerIleThrLysGluThrTrpLysIle 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATAGAGCAACTTACAGACGAAATTAATAGAATT 933
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                   US-09-980-054A-12 (1-148) x US-08-500-222-1 (1-1497)
                                                                                                                                                                                                                                                                                           40 GlyTyrGlnThrGlyPheGlnArgPheLeuIle----
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77.50
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 Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
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                                                                     Query Match:
DB:
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Squence 6062, Application US/10032585

Squence 6062, Application US/10032585

Publication No. US20030180953A1

SENERAL INFORMATION.

SAPPLICANT: Terry, Roemer D.

APPLICANT: Charles, Boone

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey

TILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

TILE OF INVENTION UNDER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE PATENTION OF SEQ ID NOS: 8000
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, April Sequence 21904, A Sequence 201, App Sequence 201, App Sequence 2058, Ap Sequence 62, App Sequence 64, App Sequence 76, App Sequence 76, App Sequence 76, App Sequence 77, App Sequence 77, App 1
 Sequence 6062, Ap
Sequence 171, Ap
Sequence 171, Ap
Sequence 5171, Ap
Sequence 7171, Ap
Sequence 7171, Ap
Sequence 7171, Ap
Sequence 56991, A
Sequence 24748, A
Sequence 158, Ap
                                                                                                                                        Sequence 163, App
Sequence 44827, A
Sequence 24958, A
Sequence 24958, A
Sequence 289, App
Sequence 21, Appli
Sequence 6127, Ap
Sequence 6260, Ap
Sequence 6260, Ap
Sequence 6355, Ap
Sequence 4355, Ap
Sequence 4355, Ap
Sequence 4355, Ap
Sequence 24731, A
Sequence 24731, A
Sequence 2671, App
Sequence 217, App
Sequence 2117, App
Sequence 2117, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 77, App
Sequence 6585, A
Sequence 42952,
13 US-10-032-585-6062
15 US-10-128-714-6171
15 US-10-128-714-6171
15 US-10-128-714-6171
15 US-10-128-714-6171
15 US-10-032-585-2884
15 US-10-032-585-2884
15 US-10-032-585-2884
17 US-10-032-585-3062
18 US-10-032-585-3062
19 US-10-369-493-24748
10 US-09-932-183A-1
10 US-09-932-183A-1
11 US-10-369-493-44624
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13 US-09-918-585-586
13 US-09-918-585-586
14 US-10-369-493-4556
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16 US-10-369-493-4556
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18 US-09-815-242-807
19 US-09-815-242-807
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11 US-10-398-221-2058
12 US-10-398-221-2058
12 US-10-014-0997-62
12 US-10-014-0997-62
12 US-10-014-0997-76
13 US-10-014-0997-76
13 US-10-014-0997-76
13 US-10-014-0997-77
13 US-10-014-0997-77
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1934
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, ORGANISM: Candida albicans
US-10-032-585-6062
                                                                                                                                                                                                                                                                                                                                                                                                                 1230025
                                                      US-10-032-585-6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.5
78.5
778.5
78.5
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119.5
119.5
106.5
99.5
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      Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-DE-published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCLE -LOOPEXT=0 -UNITS=bits -START=1 -RND=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc -NORM=ext -HRAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09980054 @CGN 1 1 391 @runat 13022004 163843 26438
-NOFUG=6 -ICOPUS 3 -NO WAAP -LARGEQUERY -NGG SCORS=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOTT=120 -WARN TIMEOTT=30 -THREADS=1 -KGAPOP=10 -XGAPEXT=0.5
                                                                                          February 16, 2004, 15:27:53 ; Search time 332 Seconds (without alignments) 1642.101 Million cell updates/sec
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                                                                                                                                            US-09-980-054A-12
772
1 MSDIDIDNVLNLEEEQYELG..........NLVKEVGGTLQVSENPDDMW 148
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(c) 1993 - 2004 Compugen Ltd
                                                                    nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
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Maximum DB seq length: 200000000
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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1447

Length: Matches:

9.01e-87 764.00

Alignment Scores: Pred. No.:

Description

Query Match Length DB

Score

Result No.

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of Essential Genes in Aspergillus fumigatus and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 CCTCTCCCCTCCAGTTCACGCCTGCCAAAACCTCGAGATTCTACTCGAATTAGTTGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGluLysAsnIle 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 CCAGCTTCGTTGCCTATGGAGAACACGGAAGAAGCTGTCACAGATGTTGATGAGCGTCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 GCAGACTCTGAAATCTCTCGGAATTCGTCACAGGAGAGTGACGGAACAGATACCCGCAAA 300
                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                          46 GlnArgPheLeullelleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSerHisIle 65
                                                                                                                                                                                                                                6 IleAspAsnValleuAsnLeuGluGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGln 25
                                                                                                                                                                                                                                                                                                                              26 IleGingiyThrLysAspGinTyrLeuGjuGiyLysGluTyrGiyTyrGinThrGiyPhe
                                                                                                                                                                                                                                                                                                                                                                  479 ACTGACGGTGCCCAGGCTGGTTACACTGAAGGAAGCGTGTTTGCCGTTGAGAAAGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMet---
                    2877
24
27
24
34
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                                                                                                                                                                                       US-09-980-054A-12 (1-148) x US-10-128-714-6171 (1-2877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AspGlnTyrAsn------
                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGGGCGCTGAATCAAGGCCAAGCTTATC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Alang, Bo
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alaxey M
APPLICANT: Ensekin, Alaxey M
APPLICANT: Ensekin, Methods of Use
TITLE OF INVENTION: Identification of Essent
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PLING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 171, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION:
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119.50
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                                                                       Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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LENGTH: 3863
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APPLICANT: Hu, Wengi
APPLICANT: Tishoff, Daniel
APPLICANT: Tishoff, Daniel
APPLICANT: Tishoff, Daniel
APPLICANT: Tishoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lamielax, Sabastien
APPLICANT: Lamielax, Sabastien
APPLICANT: Lamielax, Sabastien
APPLICANT: Lamielax, Sabastien
APPLICANTON: Methods of Use
FILE REFERENCE: 10182-018-999
FILE REFERENCE: 2002-04-23
CURRENT APPLICATION NUMBER: US 60/285,697
FRIOR FILING DATE: 2001-04-27
FRIOR PELICATION NUMBER: US 60/287,066
FRIOR FILING DATE: 2001-06-05
FRIOR PELICATION NUMBER: US 60/295,890
FRIOR FILING DATE: 2001-06-05
FRIOR PELICATION NUMBER: US 60/303,899
FRIOR FILING DATE: 2001-06-05
FRIOR PELICATION NUMBER: US 60/316,362
FRIOR FILING DATE: 2001-06-03
FRIOR PELICATION NUMBER: US 60/316,362
FRIOR FILING DATE: 2001-08-31
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                            Mismatches:
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SOFTWARE: PatentIn version 3.1
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US-10-128-714-6171/c
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APPLICANT Terry, Roemer D.
APPLICANT Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPREBENCE: 10.182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: AD001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 2884
LENGTH: 65
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1419 GAAAAGTTTCTTGAATTGGGAAGACTATATGGCAAAGCACTCGTCTGGGCCCCAGAGGCTC
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1119 AAGGCGCTGCAATCAAGGCCAAGCTTATC 1090
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Publication No. US20030180953A1
GENERAL INFORMATION:
        ; SEQ ID NO 5171

; LENGTH: 4877

; TYPE: DNA

; CRGANISM: Aspergillus fumigatus

US-10-128-714-5171
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APPLICANT: Examidio, Carlos
APPLICANT: Excankin, Alexey M
APPLICANT: Expandio, Carlos
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
FILE REFERENCE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR SPELICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
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... Sequence 5171, Application US/10128714
... Publication No. US20030119013A1
... GENERAL INFORMATION:
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-171
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                                                                    Alignment Scores:
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| Sequence 56991, Application US/10242535A | Publication No. US/20040013663A1 | GENERAL INFORMATION | GENERAL INFORMATION | GENERAL INFORMATION | GENERAL INFORMATION | C. US/102040013663A1 | GENERAL INFORMATION | C. US/102040 | C. 
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                                                                                278 AICTCAGCCATATAATGAGGGTGATCTTCTTTGGAACCATTCGTATGCAAGGAGATGCG
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: usang, no APPLICANT: usang, no APPLICANT: usang, no APPLICANT: Tishkoff, Daniel APPLICANT: Tishkoff, Daniel APPLICANT: Tishkoff, Daniel APPLICANT: Tishkoff, Daniel APPLICANT: Zamudio, Carlos APPLICANT: Lemieux, Sebastien M TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and TITLE OF INVENTION: Methods of Use FILE REFERENCE: 10182-018-99 CURRENT APPLICATION NUMBER: US 60/285,697 PRIOR APPLICATION NUMBER: US 60/285,697 PRIOR APPLICATION NUMBER: US 60/287,066 PRIOR APPLICATION NUMBER: US 60/287,066 PRIOR APPLICATION NUMBER: US 60/287,066 PRIOR APPLICATION NUMBER: US 60/303,899 PRIOR PILING DATE: 2001-06-05 PRIOR FILING DATE: 2001-06-05 PRIOR FILING DATE: 2001-06-05 PRIOR FILING DATE: 2001-06-31 PRIOR FILING DATE: 2001-08-31 PRIOR PRIOR FILING DATE: 2001-08-31 PRIOR APPLICATION NUMBER: US 60/303,899 PRIOR APPLICATION NUMBER: US 60/303,899 PRIOR APPLICATION NOMBER: US 60/303,8
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397 GAAAAGTITCTIGAATIGGGAAGACTATAIGGCAAAGCACTCGICIGGGCCCAGAGGCIC 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 IleAspAsnValleuAsnLeuGluGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGln 25
                                                                                                                                                                                            SerAspileAspileAspAsnValLeuAsnLeuGluGluGluGlnTyrGluLeuGlyPhe 21
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                                                                                                                                                                                                                                   ----SerHisIleAspGlnTyrAsnAsnSerSerLeuArgAsnHis---
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Matches:
Conservative:
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Mismatches:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Aspergillus fumigatus US-10-128-714-7171
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Sequence 158, Application US/10171581

Sublication No. US20030104426A1

SERVERAL INFORMATION:

APPLICANT: Dai, Hongrue

APPLICANT: Mac Mac

TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia

FILE REFERENCE: 9301-157-999

CURRENT APPLICATION NUMBER: US/10/171,581

CURRENT APPLICATION NUMBER: US/10/171,581

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2001-66-18

NUMBER OF SEQ ID NOS: 366

SEQ ID NO 158

LENGTH: 5967
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1489 GAAGTTGAAGGAAATGCCCACTATGTAAAACACCCAATAGAT 1530
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Matches:
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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DATABASE ENTRY DATE: 2001-06-18
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US-10-171-581-158
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DB:
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                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Xianfeng
TITLE OF INVENTION: Expression OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPRESENCE: 38-10 (52052)8
FILE REPRESENCE: 38-10 (52052)8
PRIOR PAPLICANTON NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 24748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 ACTATTAAAGATTTGCTTGAAGAACTTAAAAATCTAAATGAAGAGATTGAAAAAAATTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1144 AAATATAAAAGAATATGTGAAGAGTGCAAAGAATAC------TATGAGAAG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1309 AAACTITIAGAAGAAACAAAAAATATIGACATIGAAAGTATIGAAATICATTAAAAGAG 1368
                                                              97 ValGluAspTyrGluLys-----AsnIleLysLysAlaArgAsnLysLeu---Arg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 ValileAlaSerileThrLysGluThrTrpLysIleAspSerLeuAspAsnLeuValLys 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 -------LeuGluGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGlnIleGln 27
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                            48 PheLeu---IlelleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSerHislleAsp
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Mismatches:
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                                                                                                                                                                                                     Sequence 24748, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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CRGANISM: Methanococcus jannaschii
US-10-369-493-24748
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Best Local Similarity:
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Pred. No.:
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Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
        5797 GAAGAACAAAAGAAAGCTGCGAAAGGTTTCCCTGACATCCAGGAACAGATCACTGAAGAA 5856
                                                                                                                                                                                                                                                                                                           5004 GAAGCGCATCAGAAAGCGACTCAAGACTTG-----ATCGATGAGATAGACAAGACTGAT 6057
                                                                                                                                                                                                                                   ...-----TACAAAGATGTACGAAAAATGCGTGATATTGAGTTA 6003
                                                                                                                                                                                               93 GlyAspLysGluValGluAspTyrGluLysAsnIleLysLysAlaArgAsn---LysLeu 111
                                                                                                                                                                                                                                                                       112 ArgvalileAlaSerileThrLysGluThrTrpLysIleAspSerLeuAspAsnLeuVal 131
                                                                              8857 ATGCAAAACTGGAAAGATAAACAGAAAGATTTTAACCTTGAGCTTTATAACACCAAGAAG
                                                  MetlysPheTrpLeuSer-------HislleAspGlnTyrAsnSerSer
                                                                                                                        SerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAlaGlnIleSerIleThrAsn
                                                                                                                                              132 LysgluValGlyGlyThrLeuGlnValSerGluAsnProAspAspMet 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
FILING DATE: 04-May-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 163:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Scies
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 163, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
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STRANDEDNESS: double
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LENGTH: 6723 base
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2144 CATCTGCGCCAAACAATTCAGTCTCTACGACGACGACAGTTTAGTGGAGGTTTACCCTTGGCA 2203
                                                                                                                                      2084 CTTGATGAAAAAGAACAGGCTCTCTATTATGCTCGTTTGGAGGGAAGAAACAGAAAA 2143
                                                                                                                                                                                                                                                                                                                                       95 LysGluValGluAspTyrGluLysAsnIleLysLysAlaArg---AsnLysLeuArgVal 113
                                                                                                                                                                                                                                                                                                                                                                                                                114 IleAlaSerIleThrLysGluThrTrpLysIleAspSerLeuAspAsnLeuValLysGlu 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspileAspAsnValLeuAsnLeu---GluGluGluGlnTyrGluLeuGlyPheLysGlu 23
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                                                                                                                                                                                       GingluLeuMetLysPheTrpLeuSerHisIleAspGlnTyrAsnAsnSerSerLeu 74
                                                                                                                                                                                                                                                             75 ArgAsnHisleuAsnAsnLeuGluAspIleMetAlaGlnIleSerIleThrAsnGlyAsp 94
                                                                                                              --IleGlyTyrIle 54
                                      --- ileGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGly
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APPLICANT: Estell, David A.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394C1-US
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/932,183A
CURRENT PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/308,375
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: EP9719636.4
PRIOR APPLICATION NUMBER: EP9719636.4
PRIOR APPLICATION NUMBER: EP9719636.4
PRIOR APPLICATION NUMBER: EP9719636.4
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FREESEQ for Windows Version 3.0
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                                                                                                              TyrGlnThrGlyPheGlnArgPheLeuIle
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Best Local Similarity:
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st Local Similarity: 32.94	DD 61 CIGGAAGAAGITCICAAIAGITCCGGIGACAAGICCAAGGCIGAAITGGAAAAACIACGI 120 QY 105 LysLysAlaargAsnLysLeuargVallleAlaSerileThrLysGluThrTrpLysIle 124	Oy 140 ValSerGluAsnBro 144 Db 226 GTTCGTGACAATCCG 240 RESULT 14 US-10-359-44024 C 200-370-370-370-370-370-370-370-370-370-3		TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52.05.2) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR PILLING DATE: 2002-02-01 NUMBER OF SEQ ID NOS: 47374	; SEQ ID NO 44024 ; LENGTH: 2637 ; TYPE: DNA ; ORGANISM: Pyrococcus horikoshii US-10-369-493-44024	Alignment Scores: 5.09 Length: 2637 Pred. No.: 83.50 Matches: 37 Score 41.18 Conservative: 40 Best Local Similarity: 19.79 Mismatches: 61 Query Match: 10.82 Indels: 49 DB: 12 Gaps: 6	US-09-980-054A-12 (1-148) x US-10-369-493-44024 (1-2637) QY	36 1651 44
Pred. No.: Score: 6723 11.1 Length: 6723 46 Score: Similarity: 40.00% Conservative: 20 Best Local Similarity: 11.08% Mismatches: 62 Query Match: 11.08% Mismatches: 62 DB: 10.09-980-054A-12 (1-148) x US-09-070-927A-163 (1-6723) Cy 3 GluGluGluGluTyrGluLeuGlyphelysGluGlyGlnIleGln 27 Db	28 GlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGly 4322 TTTGAAGGATAAGCAAATCAAGCTCTCTGAAATTCGAGAAAAAGGCATTCAAAATAAC 45 PheGlnArgPheLeullelleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSerHis	Oy 65 IleaspdintyrananberSerSerLeuargasnHisLeuAsnasn 80	Qy 90 11eThrAsnGlyAspLysGluValGluAspTyr 100 bb 4091 ACTGAAAAATTCAACTATCACTAAAGAAATAAAAAATTGCAAGAGTACATTACTCAA 4032 Qy 101GluLysAsnIleLysLysAlaAtgAsnLysLeuArgValIleAlaSerIleThr 118 Db 4031 AGTAACGAAGCTATTCTAGAACTTCCGCTAAACAAGTGAGATTACAGAATAGAT 3972	119 LysGluThrTrpLyslleAspSerLeuAspAsnLeuValLysGluValGlyGlyThrLeu	RESULT 13 US-10-369-493-44827 ; Sequence 44827, Application US/10369493 ; Publication No. US20030233675A1 ; GENERAL INFORMATION:	APPLICANT: Cao, Yongwei APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Serven C. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES TITLE OF INVENTION: 20.10/200201	CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT PILING DATE: 2003-02-28 FRIOR FILING DATE: 2002-02-1 FRIOR FILING DATE: 2002-02-1 SEQ ID NO 44827 LENGTH: 255 TYPE: DNA CREANTEM: A PROPERTY PARTY	ט אי

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205)8
FURENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                          GluValGlu-----AspTyrGluLysAsnIleLysLysAlaArgAsnLysLeuArg 112
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                                                                                                                                           -----SerileThrAsnGlyAspLys 95
                                  51 IleGlyTyrileGlnGluLeuMetLysPheTrpLeuSerHisIleAspGlnTyrAsnAsn 70
                                                                                       SerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAlaGlnIle-----
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Matches:
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local Similarity:
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LENGTH: 2640
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1711 GAATTATCTGAGATCGAAGATAGGTTACTAAGGTTGGGATTTAAAACAATAGATGAGCTT 1770
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---GlyPheGlnArgPhe---LeuIle
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completed: February 16, 2004, 17:23:44 he : 352 secs time

DNA encoding a Can Candida albicans e Candida albicans e Probe for DNA enco

Description

and is derived by analysis of the total score distribution

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Human polynucleoti Human secreted pro Human colon cancer

Human polynucleoti DNA encoding novel

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Borrelia burgdorfe Drosophila melanog

Human chromosome

Human colon cancer

Enterococcus Interococcus

Bacillus subtilis

Borrelia burgdorfe Plasmodium falcipa

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CaDRA472; CaDR489; ICaDR527; 2CaDR527; CaFLO24; CaNL260; CaDR361; antifungal; fungal infection; pathogenic fungi; 86.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene identification; essential gene; GRACE; pathogenic fungus; gene replacement and conditional expression; fungal infection; ds.
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P-PSDB; AAU15103.
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allele
                                          21 TATCAAACTGGATTTCAACGATTTTAATCATTGGTTATATTCAAGAATTAATGAAATTT
                                                                                                                                                                                                             181 TGGTTATCCCATATAGATCAATAATAACTCTTCTTCACTTCGGAATCATTTGAATAAT
                                                                                                                                                                                                                                                                                                  GAAAAAATATTAAAAAGGCAAGAAAAATAAAATTAAGAGTGATAGCTAGTATAAAGAA
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                  TyrGlnThrGlyPheGlnArgPheLeuIleIleGlyTyrIleGlnGluLeuMetLysPhe
                                                                                                   TrpLeuSerHisIleAspGlnTyrAsnAsnSerSerSerLeuArgAsnHisLeuAsnAsn
                                                                                                                                                                                    LeuGluAspileMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyr
                                                                                                                                                                                                                                                                     GluLysAsnIleLysLysAlaArgAsnLysLeuArgValIleAlaSerIleThrLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fungus, yeast, tetracyclin, promoter, GRACE strain, blosynthesis, signal transduction, DNA replication, cell division, growth, proliferation, Candida albicans, fungicide, antifungal, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructing strains for identifying gene products as effective for therapeutic intervention, by inactivating in the strain one of a gene and placing other allele of the gene under conditional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 37; SEQ ID NO 6062; 167pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans essential gene SEQ ID NO 6062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 AGTGAAAACCCCGATGATATGTGG 444
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20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
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RESULT
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cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the virulence of a diploid fungus to an artifuugal agent that inhibits the growth of a fungus and refungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modilates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treatms infection by C. albicans. The present sequence is that of an essential Candida albicans gene used in the method of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGluAspIleMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PhelysGluGlyGlnIleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe for DNA encoding a Candida albicans protein CaNL260
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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RESULT 5
ABT20223/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                              The present sequence represents a probe for DNA encoding a Candida albicans protein. The specification describes genes CaDRA472, CaDR489, ICADR527, CaPL024, CaNL260, and CaDR361. These genes are essential for survival, and so are good targets for antifungal agents. The Candida albicans genes and their derived proteins are used to screen compounds for the ability to inhibit the activity of the protein, i.e. for antifungal activity. The proteins are also used to generate a protective antibody response against fungal infections in mammals. The candida albicans proteins and genes, and their antibodes, are used for diagnosing fungal infections, specifically C. albicans (in standard amplification, hybridisation or immunological assays, and for studying
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                                                                                                                                                                                                   proteins,
for drug
                                                                                                                                                                                               New polynucleotides from Candida albicans and their derived useful for diagnosis and treatment of fungal infections and
antifungal; fungal infection; pathogenic fungi; probe; ss.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                             Example 5; Page 85-86; 89pp; French
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                                                                                                                                 (HMRI ) HOECHST MARION ROUSSEL,
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100.00%
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                                                                                                            99FR-0007250.
                                                                                      08-JUN-2000; 2000WO-FR01567
                                                                                                                                                       Lalanne J, Rocher C;
                                                                                                                                                                            WPI; 2001-050024/06.
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Best Local Similarity:
                      Candida albicans
                                                                                                                                                                                                                                                                                                                                                                               amplification, h
pathogenic fungi
                                          WO200075305-A2.
                                                                                                           1999. - NUL-60
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic corganism such as A. fumigatus, to treat a non-infections by abathogenic corganism such as A. fumigatus, to treat a non-infection disease in a subject (e.g. cancer), to prevent or inhibit formation on a surface of a blofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or expressing recombinant protein for characterisation, screening or expressing incomprising with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or corganisms invede or reside, for comparing with the DNA sequence of or their related or distant pathogenic organisms to identify similar biochemical activity and/or function, for comparing with DNA corporates of other related or distant pathogenic organisms for attachment to a nucleic acid array for examination of expression patterns, for radialng anti-protein artipodies, as an organism to radial activity and polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding correct organism invade or reside, and for identifying polynucleotides encoding the other protein corganism invade or reside, as a marker for content or the protein in biological fluids, as a marker for content or the polypeptides or to elect the case or virulence organism. This solvential which pathogenic organism invade or reside, and expension organism invade or veside, and expension organism invade or veside, and marker for factors. This polynucleotides expenses the expression organism invade or veside, and marker for factors.
                                                                                                                                                                                                                                                                                                                Fungicide, cytostatic, essential gene, Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response; ds.
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Aspergillus fumigatus, useful for treating or preventing infections
A. fumigatus, or for treating a non-infectious disease in a subject
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genes of Aspergillus fumigatus of the invention.
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                                                                                                                                                                                                                                    Aspergillus fumigatus essential gene #2581
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ABT20223 standard; DNA; 2877 BP
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40.67%
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05-JUN-2001; 2001US-295890P.
09-JUL-2001; 2001US-303899P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus
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us-09-980-054a-12.rng

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                                                                                                                                                                                                                                                                299 TCTCAGCCATATAATGAGGGTGATCTTCTTTGGAACCATTCGTATGCAAGGAGATGCTG 240
                                                                                                                                                                                                                                                                                                                                                359 GCAGACTCTGAAATCTCTCGGAATTCGTCACAGGAGAGAGGGGAACAGAAAACCCGCAAA 300
                                                                                                                                                                                                                                                                                                                                ---AlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGluLysAsnIle 104
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                                                                6 IleAspAsnValLeuAsnLeuGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGln 25
                                                                                                                                                      46 GlnArgPheLeuIleIleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSerHisIle 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds.
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Aspergillus fumigatus, useful for treating or preventing infections by
                                                                                                          26 IleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPhe
                                                                                                                                                                                                                                             ---AspGlnTyrAsn------
                                                                                                                                                                                                                                                                                       -----AsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMet---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hu W,
   448
341
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 Mismatches:
Indels:
Gaps:
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                                           US-09-980-054A-12 (1-148) x ABT20223 (1-2877)
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat a non-infectious by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or cherapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify optential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein artibodies, as an of expression patterns, for raising anti-protein artibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding cure action. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polynucleotide sequence represents one of the essential
or for treating a non-infectious disease in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3863 BP; 983 A; 980 C; 970 G; 930 T; 0 other;
                                                                                English.
                                                                                -; 175pp;
                                                                                Disclosure; Page
A. fumigatus,
                               e.g. cancer
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3863 344 277 341 3 Length:
Matches:
Conservative:
Mismatches:
Indels: 0.00123 119.50 40.678 22.678 15.488 Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: DB: .. No.:

US-09-980-054A-12 (1-148) x ABT17813 (1-3863)

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438 617 ACTGACGGTGCCCAGGCTGGTTACACTGAAGGAAGCGTGTTTGCCGTTGAGAAAGGCTTC 558 :::::|||||| :::||||| :::||| :::||| ::: TCTCAGCCATATAATGAGGGTGATCTTCTCTTGGAACCATTCGTATGCAAGGAGATGCTG 378 377 CCTCTCCCCTCCAGTTCACGCCTGGCCCAAAAACCTCGAGATTCTACTCGAATTAGTTGAT 318 ---AlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGluLysAsnIle 104 CCAGCTTGCTTAGCCTATGGAGAACACGGAAGAAGCTGTCACAGATGTTGATGAGAGGTCTT 258 65 69 25 45 GlnArgPheLeulleIleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSerHisIle 65 6 IleAspAsnValLeuAsnLeuGluGluGluGluGlnTyrGluLeuGlyPheLysGluGlyGln 497 GCAGACTCTGAAATCTCTCGGAATTCGTCACAGAGAGAGTGACGGAACAGATACCCGCAAA 26 IleGinglyThriysAspGinTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPhe ---AspGlnTyrAsn----------AsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMet---46 65 99 437 70 98

LysLysAlaArgAsnLysLeuArgValIle 114

Conservative: Mismatches: Indels:

0.00166 119.50 40.67% 22.67% 15.48%

> Percent Similarity: Best Local Similarity:

No.:

Query Match:

Gaps:

Length: Matches:

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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fundatus. The isolated nucleic acids of the invention are used to treat a non-infectious by a pathogenic organism such as A. fundatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object organism such as A. fundatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fundatus. The polynuclectides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential or virulence genes, for selecting and sequences of other related or distant pathogenic organisms to identify protein antibodies, as an axingen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein antipodie, as a mineraction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence to sections. This polymulectice sequence represents one of the essential
                                                                                                                                                                                                                                                   Pungicide, cytostatic, essential gene, Aspergillus fumigatus, infection,
cancer, contamination, biofilm, antibody; immune response; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections A. fumigatus, or for treating a non-infectious disease in a subject
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Aspergillus fumigatus essential gene #1985.
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05-JUN-2001; 2001US-295890P.
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Alignment Scores:

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                                1479 ACTGACGGTGCCCAGGCTGGTTACACTGAAGGAAGCGTGTTTGCCGTTGAGAAAGGCTTC 1420
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                 GlnArgPheleulleIleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSerHisIle
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                                                                26 IleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPhe
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08-APR-1999;
16-APR-1999;
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WPI; 1999-081217/07.
                                    Borrelia burgdorferi
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Best Local Similarity:
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22-JUL-1997;
22-JUL-1997;
                                                    WO9858943-A1.
                                                                                       18-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 IleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                46 GlnArgPheLeullelleGlyTyrileGlnGluLeuMetLysPheTrpLeuSer----
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32
22
51
18
                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                Length:
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       99US-0159331.
99US-0159637.
99US-0159638.
                                 99US - 0.159584

99US - 0.160741

99US - 0.160767

99US - 0.16076

99US - 0.160814

99US - 0.160814

99US - 0.160818

99US - 0.161408

99US - 0.161408
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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                                                                                                                                                                                                                              0.000848
116.00
43.90%
25.02%
15.03%
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Best Local Similarity:
                                 18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                                                               25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
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                                                                    -OCT-1999
                                                                             -OCT-1999
                                                                                                       22-OCT-1999
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DB;
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1581 GAACTTCTTGAAAGTCAAACAGATTTGATTAATAAGCTTTTAAAAAAATATAAACAATTA 1640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 -------PheleullelleglyTyrileGlnGluLeuMetLysPheTrpLeuSer 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 HislleAspGlnTyrAsnAsnSerSerLeuArgAsnHisLeuAsnAsnLeuGluAsp 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrella burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterization, prevention and therapy of Bb infections, e.g. Lywe disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrella belongs to a family of motile, spiral-shaped bacteria called spirochetes Spirochetes are pathogenic in humans and Borrella causes epidemic andemnic relapsing fever, and Lyme borreliosis, more commonly known as
Borrelia burgdorferi, spirochete, bacterium, pathogen, Lyme disease, epidemic relapsing fever; Lyme borreliosis; infection, diagnosis, characterisation, detection, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LysGluTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith HO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2462 BP; 1080 A; 229 C; 357 G; 792 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dougherty BA, Fraser C, Lathigra R,
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Conservative:
Mismatches:
Indels:
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97US-0053344.
97US-0053377.
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us-09-980-054a-12.rng

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(ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fungicide; cytostatic; cancer; contamination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-093124/08
                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by assette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter; so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are useful for identifying a gene that cells in which both alleles of a gene are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the cutivity of a gene product, preferably enzymatic activity, carbon compound actabolism, blosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division
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---CAAAAAGACATATCTAGTTTAGATACTAAGATAGATAATGTAGAAAAGAAT 1874
                                                                                                                                    118
                                                                                                           137
84 IleMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGluLysAsn 103
                                                                                                                                                                                                                                                                                                                                                            Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional
                                                     ------IlelysLysAlaArgAsnLysLeuArgVal---IleAlaSerIleThr
                                                                                                           119 LysGlu---ThrTrpLysIleAspSerLeuAspAsnLeuValLysGluValGlyGlyThr
                                                                                                                                                                                                                                                                                                                                   Candida gene related tetracyclin promoter PCR primer SEQ ID NO 2884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 76; SEQ ID NO 2884; 167pp + Sequence Listing; English.
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20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
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                                                                                                                                                                                                                                                  ABZ28869 standard; DNA; 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-566694/60
                                                                                                                                                                  LeuGln 139
                                                                                                                                                                                                                                                                                                                                                                                                                      Candida albicans
                            AATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
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                                                                                                                                                                                             1995
                                                     104
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activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of a PCR primer used in the method of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the Buropean Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ል
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAspIleAspIleAspAsnValLeuAsnLeuGluGluGluGluTyrGluLeuGlyPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM;
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Mismatches:
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                                                                                                                                                                                                                         Sequence 65 BP; 20 A; 11 C; 2 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                   Length:
Matches:
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27-APR-2001; 2001US-287066F.
05-UUN-2001; 2001US-295890P.
09-UUL-2001; 2001US-303899P.
31-AUG-2001; 2001US-316362P.
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by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. funitar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify optential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an artising to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for isolate correlative receptors or liquads in the case or virulence factors. This polymucleotide sequence represents one of the essential

Sequence 2601 BP; 671 A; 675 C; 677 G; 578 T; 0 other;

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AsnGlyAspLysGluValGluAspTyrGluLysAsnIleLysLysAlaArgAsnLysLeu 111
                                                                                                                                                                                                                                                                               397 GARARGITICTIGAAITGGGAAGACIAIAIGGCAAAGCACICGICIGGGCCCAGAGGCIC 338
                                                                                                                                                                                                                                                                                                                                  278 ATCTCAGCCATATAATGAGGGTGATCTTCTTGGAACCATTCGTATGCAAGGAGATGCG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 ACTGACGGTGCCCAGGCTGGTTACACTGAAGGAAGCGTGTTTGCCGTTGAGAAAGGCTTC 398
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                                                                                                                                                                                                 26 IleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPhe
                                                                                                                                                                                                                                                        46 GlnArgPhereullelleGlyTyrIleGlnGluLeuMetLyBPheTrpLeu-----
                                                                                                                                                                                                                                                                                                                  ----SerHisIleAspGlnTyrAsnAsnSerSerLeuArgAsnHis-----
                                                                                                                                                                                                                                                                                                                                                                                                                               ---LeuAsnAsnLeuGluAspIleMet------AlaGlnIleSerIleThr
          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                              US-09-980-054A-12 (1-148) x ABT20821 (1-2601)
                                                                                    Gaps:
            0.024
106.50
42.66%
24.48%
13.80%
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                                         Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                        Query Match:
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ABA09167 standard; cDNA; 1131 BP

ABA09167

(first entry)

11-JAN-2002

ABA09167;

77

Human GK003 homologue-encoding cDNA, SEQ ID NO:943.

cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metatersis; cancer; timours; haematopoietic disorder; myeloid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopath; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiathmatic; antiarthritic; haemostatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.

Homo sapiens.

WO200157188-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

rang YT, Liu C, Drmanac RT

WPI; 2001-457740/49. P-PSDB; ABB11923

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 1; Page 809; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of packducing the nucleotides. Concleotide against the polypeptides, methods of detecting the nucleotides or polypeptides of the invention. Although novel, many of the bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby optential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, or known proteins, thereby care various activities, including cytokine, cell proliferation or cell differentiation activity; activity, issue growth activity; activity, activities, haemostatic, thrombotic or chemothatory activity; activities, haemostatic, thrombotic or chemothatory activity; activities, haemostatic, thrombotic or chemothatory activity; activities, propaptides and nucleotides of the invention are useful for preventing, treating or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions of promote wound creating stowth. Polypeptides involved with tissue regeneration and creating stowth. Polypeptides involved with tissue regeneration and creating stowth. Polypeptides involved with tissue regeneration and fungal infections in addition to immune disorders to remaing (e.g., of burns, indisorders (e.g., ostubing of promote cell growth. For example, such polypeptides may be used in the treatment of viral, comparation and fungal infections in addition to immune cell growth. For example, such poly

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P-PSDB; AAM79451
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Zhao QA,
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that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the disgnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
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25.44%
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Wang ZW;
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Wang D, Wang J, Zhang J, Ren F, Chen
Yang Y, Wejhrman T, Goodrich R;
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Mismatches:
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                                      03-FEB-2000; 2000US-0496914.
27-AFR-2000; 2000US-0560875.
20-UUN-2000; 2000US-0598075.
19-UUL-2000; 2000US-063936.
15-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653561.
20-CCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
2001WO-US04098
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103.50
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111 LeuArgVallleAlaSerileThrLysGluThrTrpLysIleAspSerLeuAspAsnLeu 130
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                                                                                                                                                                                                                                                                                                                                                                                                     71 SerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAlaGlnIleSerIle
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                                                                                                                                                11 AsnleugluglugluglnTyrGluLeuglyPheLysGluglyGlnIleglnGlyThrLys
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genetic analysis; diagnostic; antisense therapy; gene; ss.
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A, Lewis ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; 88.
                                                                                                                ArgAsn-Lys-----LeuArgVallleAlaSerIleThrLysGluThrTrpLys----
                                -GluLysAsnIleLysLysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5' EST, SEQ ID NO: 1970.
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Matches:
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                                GluValGluAspTyr---
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P-PSDB; AAG01966.
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Pred. No.:
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Molino GA;

Dwivedi P,

vectors

363

297

90

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from (1) can be used for determining the presence of a nucleic acid which hybridises to (1), and for determining the phenotype of cells in a sample of cells from a patient. (1) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate carractory or a solid surface, to identify a chromosome on which the corresponding gene recides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (1) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
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Sequence 677 BP; 215 A; 129 C; 166 G; 165 T; 2 other;

	677	32	23	46	19	۳	,	
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:		
	0.0284	99.50	45.83%	26.67%	12.89%	24		
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:		

US-09-980-054A-12 (1-148) x ABQ56851 (1-677)

Search completed: February 16, 2004, 14:33:36 Job time: 289 secs

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Sequence 7062, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:

APPLICANT: Recember D.

APPLICANT: Bo, Jiang

APPLICANT: Charles, Boone

CURRENT PALLICANTON NUMBER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: ParentIn version 3.1

SEQ ID NO 7062

LENGTH: 148
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; ORGANISM: Candida albicans
US-10-032-585-7062
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Best Local Similarity 98.6
Matches 146; Conservative
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Sequence 2, Appli
Sequence 11140, A
Sequence 1928, Ap
Sequence 78, Appli
Sequence 78, Appli
Sequence 1271, Ap
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Sequence 1061, Ap
Sequence 56, Appl
                                                                                                                                                                                     (without alignments)
939.048 Million cell updates/sec
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1 MSDIDIDNVLNLEREQYELG......NLVKEVGGTLQVSENPDDMW 148
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                                                                                                                                                           February 16, 2004, 14:24:58; Search time 33 Seconds
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(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

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(cgn2_6/ptodata/1/pubpaa/USO7_NBW_PUB.pep:*

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(cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-369-493-1061
US-10-198-070-55
US-10-198-070-55
US-10-369-493-21140
US-10-369-493-21140
US-10-198-070-78
US-10-198-070-78
US-10-369-493-1271
US-10-369-493-1271
US-10-159-493-1273
US-10-155-19
US-10-155-19
US-10-155-19
US-10-152-16-23
US-10-105-216-23
US-10-105-216-23
US-10-105-216-23
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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070-102 Sequence 102 42-5229 Sequence 5229 42-12125 Sequence 1212 585-7260 Sequence 726	493-61875 493-6564 493-5307 493-5308 42-13785	583-7511 Sequence 751 834-5 Sequence 5, 493-5960 Sequence 596 893-43 Sequence 43, 762-171 Sequence 171	227-202 Sequence 202 193-21954 Sequence 219 199-63 Sequence 63, 199F-67 Sequence 67, 193-1048 Sequence 758	493-11081 Sequence 110 493-5025 Sequence 502 42-11549 Sequence 1164 42-10422 Sequence 1042 493-23638 Sequence 236 42-2387 Sequence 236 42-2387 Sequence 5387	12-12869 Sequence 128 997-74 Sequence 128 182-20 Sequence 20
198 115- 115- 032		2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	982 369 014 032	S-10-369- S-10-369- -09-815-2 -09-815-2 S-10-369- -09-815-2	-815-2 -815-2 0-301- 0-037-
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ALIGNMENTS

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Length 148;

99.0%; Score 764; DB 12; Length 1. 98.6%; Pred. No. 1.5e-69; iive 2; Mismatches 0; Indels

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US-LULAGE OF APPLICATION US/10198070

Sequence 65, Application US/10198070

PUBLICATION OF US20030109437A1

GENERAL INFORMATION:

APPLICANT: AVERBACK, PAUL

APPLICANT: GEMMELL, JACK

TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION OF TOOO008

CURRENT APPLICATION NUMBER: US/10/198,070

CURRENT APPLICATION NUMBER: 60/306,161

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/306,150

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/306,150

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/331,477

PROPER APPLICATION NUMBER: 60/331,477

PROPER APPLICATION VOICES

NUMBER OF SEQ ID NOS: 125

SOFTWARR: PAGENTIN VOICES

SOFTWARR: PAGENTIN VOICES
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71 SSSLRNHLMNLED-----KNIKKARN 109
                                                                                                                                                                                                                                            19 LGFKEGQ---IQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKF-----WLSHIDQYNN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Gaps
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| Sequence 2, Application US/09932183A
| Patent No. US20020127641A1
| GENERAL INFORMATION:
| APPLICANT: Estell, David A. |
| TILLE OF INVENTION: Proteases From Gram-Positive Organisms FILE REPRENCE: GC394C1-US |
| CURRENT APPLICATION NUMBER: US/09/932,183A |
| CURRENT FILING DATE: 2001-08-17 |
| PRIOR PRILING DATE: 1999-05-14 |
| PRIOR PRILING DATE: 1999-05-14 |
| PRIOR PILING DATE: 1998-09-08 |
| PRIOR PILING DATE: 1997-09-15 |
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                                                                                                                                                                                                                                                                                                                                                                                            110 KLRVIASITKETWKIDSLDNLVKEVGGTLQVSENPDD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               892 SLR-YELLEEKSONTEDLAELIRKIGERLSLESKOEE 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : ::: | | : :: | | :::| | : :: | | : :: | | : :: | | :::| | | :::| | | :::| | :: | | :::| | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
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Best Local Similarity 24.2%; Pred. No. 6;
Matches 38; Conservative 29; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 SSSLRNHLNNLED----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-932-183A-2
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry G.
APPLICANT: Goldman, Barry G.
APPLICANT: Goldman, Barry G.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US $10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US $6/360,039
PRIOR APPLICATION NUMBER: US $6/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

Publication No. US20030109437A1

GENERAL INFORMATION:

APPLICANT: AVERACK, PAUL

APPLICANT: AVERACK, PAUL

APPLICANT: GENMELL, JACK

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF

TITLE OF INVENTION: COLDS

TITLE OF INVENTION: COLDS

TITLE OF INVENTION: CELLS

FILE REFERENCE: 59003.000008

CURRENT FILING DATE: 2002-07-19

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-07-19

PRIOR PLING DATE: 2001-07-19

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 125

SEQ ID NO 56

LENGTI 876

LENGTI 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 YLELBEKAVEYNKLTLEYITLLQEKKSIEKNINDLETRINKLLEETKNIDIESIENSLKE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FL-IIGYIQELMKFWLSHIDQYNNSSSLRNHLNNLEDIMAQI-----SITNGDKE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DID-IDNVLN-------LEBEOYELGFKEGOLOGTKDQYLEGKEYGYQTGFQR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 VEDYEK---NIKKARNKL-RVIASITKETWKIDSLDNLVKEVGGTLQVSENPDD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 24.7%; Pred. No. 2.1;
Matches 43; Conservative 34; Mismatches 62; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 876;
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11.2%; Score 86.5; DE
Best Local Similarity 24.2%; Pred. No. 5.6;
Matches 38; Conservative 29; Mismatches
                                                                                                                         Sequence 1061, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Methanococcus jannaschii
US-10-369-493-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Rattus norvegicus US-10-198-070-56
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Matches
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NUMBER OF SEC ID NOS: 3

19 LGFKEGQ----IQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKF-----WLSHIDQYNN 70

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GENERAL INFORMATION:
APPLICANT: AVERBACK, PAUL
APPLICANT: AVERBACK, PAUL
APPLICANT: AVERBACK, PAUL
APPLICANT: GENMELL, JACK
TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
TITLE OF INVENTION: CONDITIONS ENGINE
FILE REPERBACE: 5000-07-19
CURRENT APPLICATION NUMBER: 6/306,161
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PAUCHIN VOT: 2.1
SEMENT OF SEQ ID NOS: 125
SOFTWARE: PAUCHIN VOT: 2.1
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 IDQYN----NSSSLRNHLNNLEDIMAQISITNGDKEV-----
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                                                                                                                                                                                                 APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NACHIKO
APPLICANT: SCHIKAMA, TSUTOMU
APPLICANT: OTSUKA, MCTOYUKI
APPLICANT: OTSUKA, MCTOYUKI
APPLICANT: OTSUKA, MCTOYUKI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NASUHO, YASUHIKO
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: 10/10/094,749
FURRENT APPLICATION NUMBER: 60/330,435
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2011-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2011-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%; Score 83.5; Dl
22.2%; Pred. No. 8.1;
tive 32; Mismatches
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25.3%;
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Best Local Similarity 22.24
Matches 35; Conservative
                                                         HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
        ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1928
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CORGANISM: Mus musculus
US-10-198-070-78
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Green C.
APPLICANT: Hinkle, Green C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPRENCE: 38-10($2052)8
FILE REPRENCE: 38-10($2052)8
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:|| ::: ||:: : ||:: : : : ||: : : | |:| | |:| | |:| |:: | | |:| |:: | |:: | |:: | |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 MKFWLS-----HIDOYNNSSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARN-KL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 IDQYNNSSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 DIDNVLNL-BEEQYELGFKEGOLGGTKDQYLEGKEYGYQTGFQRFLIIGY-----IQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                        Query Match
11.1%; Score 86; DB 10; Length 2285;
Best Local Similarity 22.4%; Pred. No. 22;
Matches 35; Conservative 34; Mismatches 61; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1965 EAHQKATQDL--İDEIDKTDDEAKFQKELKERQDSI 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 RVIASITKETWKIDSLDNLVKEVGGTLQVSENPDDM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.0%; Score 85; DB 12
Best Local Similarity 32.9%; Pred. No. 0.37;
Matches 28; Conservative 13; Mismatches
    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 DSLDNLV---KEVGGTLQ--VSENP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1928, Application US/10094749;
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISCOAL, TAKAO
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAWATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 DASDKLVDQTKEMAGRADNYVRDNP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21140, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Xenorhabdus nematophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISHIİ, SHIZUKO
YAMAMOTO, JUN-ICHI
                                                                                                                                                             ; ORGANISM: Bacillius subtilis
US-09-932-183A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493~21140
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SEQ ID NO 2
                                                                                                                          TYPE: PRT
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Sequence 21643, Application US/10369493
; Sequence 21643, Application US/10369493
; Publication No. US2000233675A1
; Publication No. US2000233675A1
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
    APPLICANT: Steer, Gregory J.
    APPLICANT: Steer, Steven C.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Chen, Xianfeng
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TITLE OF STORMER S. 2003-02-28
    PRIOR APPLICATION NUMBER: US 60/360,039
    PRIOR FILING DATE: 2003-02-28
    NUMBER OF SEQ ID NOS: 47374
    SEQ ID NO 21643
    LENGTH: 880
    TOTAL STORMER SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RVIASITKETWKIDSLDNL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEMLADVENEIBEKEAKLAKOLESKFNEBEYEEKRERLVKLEREVSSLTA---RLEBIKKS 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SITNGDKEVE---DYEKNIKKARNKLRVIASITKETWKIDSLDNLVK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GFQRF-LIIGYIQELMKFWLSHIDQYNNSSSLRNHLNNLEDIMAQI--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 880;
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                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.8%; Score 83.5; DB
Best Local Similarity 19.8%; Pred. No. 11;
Matches 37; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.8%; Score 83.5; DE ilarity 20.1%; Pred. No. 11; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ITNGDKEVEDYEKNIKKARNKL----
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20337
LENGTH: 879
                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Pyrococcus horikoshii
US-10-369-493-20337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pyrococcus abyssi
US-10-369-493-21643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 EIKSTIE 697
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Matches 38; Conserv
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| Publication No. US20030233675A1
| Publication No. US20030233675A1
| Publication No. US20030233675A1
| Publication No. US20030233675A1
| Publication No. US20030233675A1
| APPLICANT: Cao, Yongwei
| APPLICANT: Chen, Xianfeng
| APPLICANT: Chen, Xianfeng
| TILLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
| PILLE PREPERRANCE: 38-10(52022)B
| CURRENT APPLICATION NUMBER: US/10/369,493
| CURRENT APPLICATION NUMBER: US 60/360,039
| PRIOR FILING DATE: 2002-02-21
| NUMBER OF SEQ ID NOS: 47374
| SEQ ID NO 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20337, Application US/10369493
Sequence 20337, Application US/10369493
FUDIcation No. US20030233675A1
Sequence 2037, Application No. US20030233675A1
Sequence 2037, Application No. US20030233675A1
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                                                                                                                                                              723 LKFKKWMCELIQGQKQGFQEDAEMNKRNEEKKFGISGSHEDLSKFSLDKNQLAHNKQSST 782
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                                                                                           19 LGFKEGO---IQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKF-----WLSHIDQYNN 70
                                                                                                                                                                                                                                          71 SSSLRNHLINNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL
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10.8%; Score 83.5; Di
Best Local Similarity 19.8%; Pred. No. 11;
Matches 37; Conservative 40; Mismatches
                       29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            131 VKEVGGTL-----QVSENPDDM 147
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US-10-369-493-1271
                       37; Conservative
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US-10-369-493-1271
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RESULT 15
US-10-198-070-73

1 Sequence 73, Application US/10198070

2 Publication No. US20030109437A1

3 GENERAL INFORMATION:
APPLICANT: AVERBACK, PAUL

APPLICANT: APERBACK, PAUL

TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF

TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF

TITLE OF INVENTION: CELLS

FILE REFERENCE: 59003.000008

CURRENT FILING DATE: 2002-07-19

PRIOR PELICATION NUMBER: 60/306,161

PRIOR PELICATION NUMBER: 60/306,161

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-07-19

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 125

SOFTWARE: PALCHTIN Ver. 2.1

SEQ ID NO 73

LENGTH: 970

TYPE: PRI
                                                                                 71 SSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL 130
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Fublication No. US20030079243A1
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CALCIUM ION
TITLE OF INVENTION: CHANNEL (Trp6) GENE DISRUPTIONS
FILE REFERENCE: R-80
CURRENT APPLICATION NUMBER: US/10/005,216
CURRENT APPLICATION NUMBER: US 60/280,373
FRICE APPLICATION NUMBER: US 60/280,373
FRICE APPLICATION NUMBER: US 60/285,227
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883 LKEIKQDISSLRYELLEEKSQNSEDL 908
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, ORGANISM: Mus musculus
US-10-005-216-2
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Sequence 102, Application US/10153244

Publication No. USC0300144191A1

Sequence 102, Application US/10153244

Publication No. USC0300144191A1

SERNERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, TRP-PL

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, US

TITLE OF INVENTION: POLICE VARIANTS THEREOF

TITLE OF INVENTION NUMBER: US 202-05-22

PRIOR PLILNG DATE: 2002-05-22

PRIOR PLILNG DATE: 2001-05-22

PRIOR FILING DATE: 2001-05-22

PRIOR FILING DATE: 2002-03-08

NUMBER OF SEQ ID NOS: 335

SSOFTMARE: PATENTION NUMBER: US 60/362,944

NUMBER OF SEQ ID NOS: 335

SSOFTMARE: PATENTION NOS: 335

LENGTH: 930
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Publication No. US20030162189A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
FILE OF INVENTION:
IMBER: US/10/210,152

CURRENT APPLICATION NUMBER: US 60/309,544

PRIOR APPLICATION NUMBER: US 60/309,544

PRIOR APPLICATION NUMBER: US 60/309,544

PRIOR APPLICATION NUMBER: US 60/309,544

PRIOR APPLICATION NUMBER: US 60/309,544

PRIOR APPLICATION NUMBER: US 60/309,544

PRIOR PERIOR PRIOR DIOS: 320
SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 19
LENGTH: 930
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10.8%; Score 83.5; DB 12; Length 9
Best Local Similarity 25.3%; Pred. No. 12;
Matches 37; Conservative 29; Mismatches 49; Indels
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Best Local Similarity 25.3%
Matches 37; Conservative
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690 VEQIKATLR 698
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; ORGANISM: Mus musculus
US-10-153-244-102
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US-10-210-152-19
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Sequence 3553, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
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CURRENT ELIER OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
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                                               US-08-858-2074-465
US-08-160-670A-32
US-08-160-670A-32
US-08-190-802A-60
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US-08-477-346-60
US-08-477-346-60
US-08-160-670A-8
US-08-153-634-65
US-08-912-129A-55
US-08-912-129A-55
US-08-912-129A-55
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22.4%; Pred. No. 3.9;
tive 34; Mismatches
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Sequence 3553, Ap
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                                                                                                                      February 16, 2004, 14:12:37; Search time 28 Seconds (without alignments) 223.643 Million cell updates/sec
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Sequence 2, Ag
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-198-452A-171

US-09-198-452A-171

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US-09-22-99-A-3066

US-08-867-611-10

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US-08-867-611-22

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US-08-867-611-22

US-08-867-611-30

US-08-887-534A-74

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                                                                                                                                                                                                                                                                                                                                                                                    391 ILNYLKNVQEDQKDKLINKINCAINWIRDFAPEDFKFSLRSKFDNMEILEENSKKAINEL 450
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                                                                                                                                                                                                                                     Gaps
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TITLE OF INVENTION:
CLASS I-type Lysyl-trnA Synthetase
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/508,370A
CURRENT FILING DATE: 2000-03-10
PRIOR PILING DATE: 1998-09-09
RIOR PILING DATE: 1998-09-09
SOFTWARE: MS DOS: 16
SOFTWARE: MS DOS: LENGTH: 521
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10.6%; Score 82; DB 4; Length 756;
Best Local Similarity 23.0%; Pred. No. 2.3;
Matches 35; Conservative 31; Mismatches 58; Indels
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// OTHER INFORMATION: construct expressed in Example 3
US-09-508-370A-3
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PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3553
LENGTH: 756
TYPE: PRT
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3553
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Sequence 3, Application US/09508370A
Patent No. 6492131
GENERAL INFORMATION:
APPLICANT:
Dieter Soll
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Patent No. 5837485
GENERAL INFORMATION:
APPLICANT: Entian, Karl-Dieter
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ORGANISM: Borrelia burgdorferi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 KNDKTF---NLDNIE--MKQVFNNYTTKITLVEEPEKNIKLIRDSSGIAROV--ETWYST 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 FKEGQIQGTKDQYLEGKEYGYQTGFQRFL-------IGGYIQ-ELMKFWLSHIDQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 YKSFQSDLKKDLYINGT---YETNLGALINLTTSKGCGSEGIINYIYGKHLDLSISNIIQ
                                                                                                                     APPLICANT: Kaletta, Cortina
APPLICANT: Kaletta, Cortina
APPLICANT: Klein, Cora
APPLICANT: Wieland, Bernd
APPLICANT: Wipke, Thomas
APPLICANT: Supke, Thomas
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Of Chemical Compounds
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentun Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.4%; Score 80.5; DB 2;
Best Local Similarity 27.5%; Pred. No. 0.8;
Matches 36; Conservative 24; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICATION: 435
PRICATION: 435
PRICATION DATA:
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
ATTORNEY/AGRITY INFORMATION:
NAME: Besnond, Robert W.
REGISTRATION NUMBER: 32,893
REPERROYP/OCKET WINBER: 0652.0980002
TELESCOWUNICATION INFORMATION:
TELESCOWUNICATION INFORMATION:
TELESCOWUNICATION INFORMATION:
TELESCOWUNICATION STOLENGE (202) 371-2640
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
G tz, Friedrich
Schnell, No. 5837485bert
Augustin, Johannes
Engelke, Germar
Rosenetein, Ralf
Kaletta, Cortina
Klein, Cora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08466961A
Patent No. 5843709
GENERAL INFORMATION:
APPLICANT: Entian, Karl-Dieter
APPLICANT: G tz, Friedrich
APPLICANT: Schnell, No. 5843709bert
APPLICANT: Augustin, Johannes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 275 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : |:::|:
123 ISVIPNIIQEL 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.C.
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TOPOLOGY:
US-08-392-625-17
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36;
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; Pred. No. 6.8;
16; Mismatches 47; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.1%; Pred. No. 3.5;
Matches 29; Conservative 22; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TWKIDSLDNLVKEVGGTL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 ----ELSLLAREYOGIM 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-171
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.3%;
Matches 39; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 NLVKEVGGTLQ 139
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US-09-252-991A-23066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 YNNSSSLRNHLNNLEDIMAQI--SITNGDKEVEDYEKNIKKARNKLRVIASITKETW--K 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 YKSFQSDLKKDLYINGT---YETNLGALINLLTSKGCGSEGIINYIYGKHLDLSISNIIQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----IIGXIQ-ELMKFWLSHIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels 27; Gaps
                                                  APPLICANT: Klein, Cora
APPLICANT: Klein, Cora
APPLICANT: Kujek, Thomas
APPLICANT: Kujek, Thomas
APPLICANT: Kujek, Thomas
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process for the Preparation of
TITLE OF INVENTION: 42
KUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.4%; Score 80.5; DB 2;
Best Local Similarity 27.5%; Pred. No. 0.8;
Matches 36; Conservative 24; Mismatches 44;
                                                                                                                                                                                                                                     Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-UDN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,625
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/784,234
FILING DATE: 31-OCT-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 FKEGQIQGTKDQYLEGKEYGYQTGFQRFL-
                                                                                                                                                                                                                                         : Sterne, Kessler, Golde
1100 New York Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 171, Application US/09198452A
Patent No. 659294
GENERAL INFORMATION:
APPLICANT: Griffals, R.
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Benond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                     Rosenstein, Ralf
Kaletta, Cortina
Klein, Cora
Engelke, Germar
                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 amino acids
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123 ISVIPNIIQEL 133
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                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                               SIREET: 1100 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-466-961A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                       U.S.A.
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US-09-198-452A-171
                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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Sequence 23066, Application US/09252991A

Factor Vo. 6251795
Factor No. 6551795
GENERAL INFORMATION:
FAPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
FRIOR PELICATION NUMBER: US 60/074,788
FRIOR PELICATION NUMBER: US 60/074,190
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 506
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preverITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999 CURRENT FILE REFERENCE: 9710-003-999 CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 6849 SEQ ID NOS: 6849 LENGTH: 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 IDQYNNSSSLRNHLNNLEDIMAQIS----ITNGDKEVEDYEKNIKKARNKLRVIASITKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 DEVLALKSTM-----BAQLQGFKULVGTWEGK--------YQEFKKVKLSK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 -----IMAQISITNGDKEVEDYEXNIKKARNKLRVIASITKETWKIDSLD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 DNVLNLEEEQYELGFKEGQIQGTKDQY--LEGKEYGYQTGFQRFLIIGYIQELMKFWLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ----MKFWLSHIDQYNNSSSLRNHLNNLEDIMAQISITNGDKE-----VEDYEKNIKKAR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : : | | :: | | :: | | 147 QOKTLKQSDTKVDLSNIDKELNHQKSQVEAMAEQAGITNEDKDSMLKKIEDIRKQAQQAD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S DIDNVLNLEEEQYELGFKEGOLQGTKDQYLEGKEYGYQTGFQRFLIIGYIQEL----- 57
                             APPLICANT: Tal, Joseph Y.
APPLICANT: Black, Milan S.
TITLE OF INVENTION: No. 6280738-1gA Fc Binding Forms of the Group J.
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 3.4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Indels
                                                                                                                                                    Serve, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                COMPUTER SEADABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,992A

FILING DATE: 05-SEP-1997

CLASSIFICATION THORER: US 60/024,707

PILING DATE: 06-SEP-196

ATPONEY/AGENT INPOMBATION:

NAME: ESENCE/POCKET NUMBER: 32,893

REGISTRATION NUMBER: 32,893

REGISTRATION NUMBER: 32,893

REGISTRATION NUMBER: 32,893

RELEFAN: (202) 371-2600

TELEFAN: (202) 371-2600

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.1%; Score 78; DB 3 Best Local Similarity 24.0%; Pred. No. 10; Matches 36; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 NKLRVIASITKETWKIDS-----LUNLVKE 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 KKEDAEVKVREELGKLFSSTKAGLDQQIQE 236
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GUTIERREZ, ROBIN A
LESNIEWSKI, RICHARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-867-611-10
; Sequence 10, Application US/08867611
; Patent No. 6172189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVARE, SUSHIL G
DESAI, SURESH M
CASEY, JAMES M
DAILEY, STEPHEN H
DAMSON, GEORGE J
                        ai, Joseph Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-923-992A-4
                                                                                                                                                                                                CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
SENERAL INFORMATION:
                                                                                                                                                                                    STREET:
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STEWART, JAMES L RUPPRECHT, KEVIN R FUNTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT FENTION: AMTIGENS

APPLICANT: RUPPRECH TITLE OF INVENTION: TITLE OF INVENTION:

APPLICANT APPLICANT

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206 IEMLEQLRVLWYGEKIHVAVAQEVPGTGVDTPEDLDPSTNSLDSHYQDVLKEVKAAASKV 265
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10.0%; Score 77.5; DB 3; Length 496;
Best Local Similarity 20.4%; Pred. No. 3.9;
Matches 37; Conservative 22; Mismatches 67; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 IGYIQELMKFWLS---HI-------DQYNNSSSLRNHLN--
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COUNTRY: USA
CONFUTER: ELEPRA: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: STATE: 
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/572,822
FILING DATE: 24 AUG-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
PRIOR APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
PRIOR APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMINICATION:
TELEPHONE: 708-937-6368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,757
FILING DATE:
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........ 496 amino acids
TYPE: amino acids
TOPOLOGY: 1:--
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                                       Sequence 15, Application PC/TUS9206965A
GENERAL INFORMATION:
APPLICANT: DEVARE, S.
APPLICANT: DAILEY, S.
TITLE OF INVENTION: HCV SYNTHETIC PEPTIDE FROM NS1 REGION NUMBER OF SEQUENCES:
ADDRESSES: ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Indels
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US-08-500-222-2

Sequence 2, Application US/08500222

Patent No. 5643733

GENERAL INFORMATION:
APPLICANT: Robinson, John M
APPLICANT: Pilot-Matias, Tami J
APPLICANT: Pilot-Matias, Tami J
APPLICANT: Pilot-Matias, Tami J
APPLICANT: Borrelia burgdorferi antigens
; TITLE OF INVENTION: Borrelia burgdorferi antigens
; TITLE OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06965A
FILING DATE: 19920821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.0%; Score 77.5; D
Best Local Similarity 20.4%; Pred. No. 3.9;
Matches 37; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 IGYIQELMKFWLS---HI------
                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.
ZIP: 60065-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PORENESKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REPERBENCE/DOCKET NUMBER: 4834PC
TELECOMMINICATION INFORMATION:
THE TOPOLON INFORMATION:
                                                                                                                                                                                                                     E: ABBOTT LABORATORIES
ONE ABBOTT PARK ROAD
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein PCT-US92-06965A-15
                                                                                                                                                                                                                                                              CITY: ABBOTT PARK
STATE: ILLINOIS
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RESULT 10
PCT-US92-06965A-15
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146 LDAEGYALYFSRATIPWDRDRFRAEGLETVGDNFLRHLGIYGYRAGFIRRYVNWQPSPLEH 205
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206 IEMLEQLKVLWYGEKIHVAVAQEVPGTGVDTPENPSTGLMKISDPRNTSKAINFIQTTEG 265
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266 NLNEVEKVLVRMKELAVQSGNGTYSDAD-----RGSIQIEÌEQLTDEINRÌ 311
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APPLICANT: Robinson, John M

APPLICANT: Robinson, John M

APPLICANT: Pilot-Matias, Tami J

APPLICANT: Pilot-Matias, Tami J

APPLICANT: Pilot-Matias, Tami J

APPLICANT: Pilot-Matias, Tami J

APPLICANT: Hunt, Jeffrey C

TITLE OF INVENTION: Borrelia burgdorferi antigens

TITLE OF INVENTION: Borrelia burgdorferi antigens

TITLE OF INVENTION: And uses thereof

CORRESPONDENCE ADDRESS:

ADDRESSES: Abbott Laboratories

STREET: One Abbott Park Road

CITY: Abbott Park

STREET: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
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10.0%; Score 77.5; D
Best Local Similarity 19.8%; Pred. No. 3.9;
Matches 34; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION:
APPLICATION: 435
CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,704
FILING DATE: 21-0CT-1991
ATTORNEY, GGENT INFORMATION:
NAME: WONG, WEAN KHING
REGISTRATION NUMBER: 33561
REFERENCE/DOCKET NUMBER: 5051.US.0
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION INFORM
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MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Abbott Laboratories
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STRAIN: B31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                     CITY: Abbott Park
STATE: Illinois
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146 LDAEGYALYFSRATIPWDRDRFRAEGLETVGDNFLRHLGIYGYRAGFIRRYVNWQPSPLEH 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CASEX, SUSTIL GASPLICANT: CASEX, JAMES MARPLICANT: CASEY, JAMES MAPPLICANT: CASEY, JAMES MAPPLICANT: CASEY, JAMES MAPPLICANT: DALLEY, STEPHEN HAPPLICANT: DAWSON, GEORGE JAPPLICANT: GUTIERREZ, ROBIN AAPPLICANT: EISMRAT, JAMES LAAPPLICANT: STEWART, MEVINES LAAPPLICANT: STEWART, KEVIN RAPPLICANT: TITLE OF INVENTION: HEPATITIS CASSAY UTILIZING RECOMBINANT TITLE OF INVENTION: HEPATITIS CASSAY UTILIZING RECOMBINANT TITLE OF INVENTION: HEPATITIS CASSAY UTILIZING RECOMBINANT TITLE OF INVENTION: ANTIGENS NUMBER OF SEQUENCES: 59 CORRESPONDENCE ADDRESS: ABBOTT LABORATORIES STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2 CITY: ABBOTT PARK ROAD, CHAD377/AP6D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 498;
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OPERATING SYSTEM: PC-DOS/NN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.0%; Score 77.5; D
Best Local Similarity 19.8%; Pred. No. 3.9;
Matches 34; Conservative 27; Mismatches
          SOFTWARE: FREGULAL, ALTERED TOTO, TOTORERY APPLICATION NUMBER: US/07/779,704B FILING DATE: 19911021
CLASSIFICATION NUMBER: US/07/779,704B FILING DATE: H991021
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WORG, WEAR MAING REFERENCE/DOCKET NUMBER: 33561
REFERENCE/DOCKET NUMBER: 5051.US.01
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION INFORMATION:
TELECHOMOTICATION OF SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LEEEQYELGFKEGQIQGTKDQYLEGKE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Borrelia burgdorferi
STRAIN: B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08867611
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy
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ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-779-704B-2
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206 IEMLEQLRVLMYGEKIHVAVAQEVPGTGVDTPENPSTGLMKISDPRNT$KAINFIQTTEG 265
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Sequence 2, Application US/07779704B

Setent No. 595702

GENERAL INFORMATION:

APPLICANT: Robinson, John M

APPLICANT: Pilot-Matias, Tami J

APPLICANT: Hunt, Jeffrey C

TITLE OF INVENTION: Borrelia burgdorferi antigens

TITLE OF INVENTION: and uses thereof

NUMBER OF ENCURNICS: 16

CORRESPONDENCES: 16

CORRESPONDENCES: Abbott Laboratories

STREET: One Abbott Laboratories

STREET: One Abbott Park Road

CIUNTRY: USA
                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/500,125 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.0%; Score 77.5; D
Best Local Similarity 19.8%; Pred. No. 3.9;
Matches 34; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 IGYIQELMKFWLS---HI--------
                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 21-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wong, Wean Khing
REGISTRATION NUMBER: 33561
REFERENCE/DOCKET NUMBER: 5051.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LEEEQYELGFKEGQIQGTKDQYLEGKE-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: 708-937-9556
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
TYPE: linear
MOLECTLE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Borrelia burg STRAIN: B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-07-779-704B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 LDAEGYALYFSRATIPWDRDRFREGLETVGDNFLRHLGIYGYRAGFIRRYVNWQPSPLEH
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06965A
FILING DATE: 19920821
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 4834PC.02
TELEPHONE: 708-937-6365
ITELEPHONE: 708-937-6365
INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
NOT STATE AND ACID
TOPOLOGY: linear
NOT STATE AND ACID
TOPOLOGY: linear
NOT STATE AND ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.0%; Score 77; DB Best Local Similarity 23.1%; Pred. No. 3.5; Matches 30; Conservative 19; Mismatches
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Job time : 31 secs
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206 IEMLEQLRVLWYG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein PCT-US92-06965A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 NKLRVIASIT 118
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GENERAL INFORMATION:
APPLICANT: DEVARE, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
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APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
APPLICANT: ABOUTT LABORATORIES
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PRIOR APPLICATION NUMBER: US/US/1/9,896
PRIOR APPLICATION DATA:
APPLICATION UNDMAR:
APPLICATION UNDMAR:
APPLICATION UNDMAR:
APPLICATION UNDMAR:
APPLICATION UNDMAR:
APPLICATION UNDMAR:
APPLICATION UNDMAR:
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APPLICATION UNDMAR:
ATORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 4834.US.P6
TELERPAN: 708-937-9556
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                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,757
FILING DATE:
APPLICATION NUMBER: US/08/179,896
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STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: ILLINOIS
COUNTRY: U c
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 30; Conserva
                                                        FILING DATE: 02
CLASSIFICATION:
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Drosophila melanog

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Staphylococcus aur
Arabidopsis thalia
Candida albicans e
S. epidermidis ope
Staphylococcus epi
Plasmodium falcipa
Salmonella typhi c
Propionibacterium
Streptococcus poly
Streptococcus poly
Streptococcus poly
Borrelia burgdorfe
                                                                                                                                                                                                                                                                           Drosophila melanog
Mutant C-beta prot
Plasmodium falcipa
Candida albicans e
Drosophila melanog
Amino acid sequenc
Helicobacter pylor
H. pylori GHPO 504
Amino acid sequenc
Amino acid sequenc
                              Drosophila melanog
Clostridium diffic
B. burgdorferi ant
B. burgdorferi ant
Bacillus subtilis
Plasmodium falcipa
Putative P. abyssi
Human transient re
Amino acid sequenc
Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides from Candida albicans and their derived proteins, useful for diagnosis and treatment of fungal infections and for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CaDRA472; CaDR489; 1CaDR527; 2CaDR527; CaPLO24; CaNL260; CaDR361; antifungal; fungal infection; pathogenic fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a Candida albicans protein CaNL260.
                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                            ABP30175
ABP26844
AAY04366
                                                                           AAB18173
AAB18173
AAB96332
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AAG82994
ABP38708
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ABP73674
ABB58792
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AAU38192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB30859 standard; Protein; 148
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  08-JUN-2000; 2000WO-FR01567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
 Lalanne J, Rocher C;
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N-PSDB; AAC86750.
 Candida albicans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200075305-A2.
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  Amino acid sequenc
Protein encoded by
Candida albicans e
Arabidopsis thalia
Novel human diagno
Human protein SEQ
Human protein SEQ
Human secreted pro
                                                                         .; Search time 39 Seconds (without alignments) 602.347 Million cell updates/sec
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| SIDSI/Geddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/Geddata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/Geddata/geneseq-embl/AA1981.DAT:*
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1 MSDIDIDNVLNLEEEQYELG......NLVKEVGGTLQVSENPDDMW 148
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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AAU15103
ABP73225
AAG30345
ABG28105
ABB11923
AAM79451
AAM78467
AAG01966
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Gapop 10.0 , Gapext
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Maximum DB seq length: 2000000000
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                     Copyright
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Match
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Result No.

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WLSHIDQYNNSSSLRNHIANLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to constructing (MI) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an
          essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutant organisms referred to as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, Aspergillus fungatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAUI5053-AAUI5113 represent proteins encoded by C. albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional
                                                                                                                                                                                                                                                                                                           1 MSDIDIDNVLNLEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKF
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                                                                                                                                                                                                            99.0%; Score 764; DB 22; Length 148; 98.6%; Pred. No. 1.5e-70; ive 2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 44; SEQ ID NO 7062; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida albicans essential protein SEQ ID NO 7062.
for therapeutic agents, for creating a
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20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
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N-PSDB; ABZ31775.
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nes 146; Conserv
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Matches
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ABP73225
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                                                          The present sequence represents a Candida albicans protein. The specification describes genes CaDRA472, CaDR489, 1CaDR527, 2CaDR527, CaNL260, and CaDR361. These genes are essential for carload, CaNL260, and CaDR361. These genes are sesential for candida albicans genes and their derived proteins are used to screen compounds ablicans genes and their derived proteins are used to screen compounds antibugal activity. The proteins are also used to generate a protective antibody response against fungal infections in mammals. The Candida albicans and genes, and their antibodies, are used for diagnosing fungal infections, specifically C. albicans (in standard amplification, hybridisation or immunological assays, and for studying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel methods for constructing fungal strains useful for identification and validation of gene products as
                                                                                                                                                                                                                                                                                                                                                                                                            1 MSDIDIDNYLNLEBEQYELGFKEGQIQGTKDQYLEGKEYGYQYGFQRFLIGYIQELMKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying genes essential to fungal metabolisms and identifying potential therapeutic agents that target these genes -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        essential gene; GRACE; pathogenic fungus; conditional expression; fungal infection.
                                                                                                                                                                                                                                                                                                                  Length 148;
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                                                                                                                                                                                                                                                                                                                  100.0%; Score 772; DB 22; 100.0%; Pred. No. 2.3e-71;
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                 Claim 11; Page 78-79; 89pp; French
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                                                                                                                                                                                                                                                                                                                                                   Matches 148; Conservative
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gene replacement and
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                   pathogenic fungi
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     16-APR-1999

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23-APR-1999

23-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

40-MAX-1999

60-MAX-1999

60-MA
         expressible selectable marker and modifying other allele by
recombination, of a promoter replacement fragment with a heterologous
promoter, so that expression of the second allele is regulated by the
promoter. [Mi] is useful for constructing a strain of diploid fungal
cells in which both alleles modified are useful for identifying a gene that
cells having both alleles modified are useful for identifying a gene that
is essential to the survival or growth of a fungus, a gene that
contributes to the virulence and/or pathogenicity of a fungus, a gene
that contributes to the resistance of a diploid fungus to an antifungal
agent, an antifungal agent that inhibits the growth of a diploid fungus
and for identifying a therapeutic agent for treatment of a mammalian
clisease. [MI] is useful for identifying a compound which modulates the
activity of a gene product, preferably enzymatic activity, carbon
cativity. The method is useful for identifying a compound having the
activity. The method is useful for identifying a compound having the
activity. The method is useful for identifying a compound having the
activity. The sequence data for modification and cell division
activity. The sequence data for this patent is not represented in the princed
sesential Candida albicans protein used in the method of the invention.
Note: The sequence data for this patent is not represented in the princed
the Buropean Patent Office.
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99US-0123180.
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99US-0126264.
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Best Local Similarity 98.67
Marches 146; Conservative
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06-APR-1999;
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09-MAR-1999
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29-MAR-1999
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PR 19-VW-1999) 9918-0144334.

PR 20-VW-1999) 9918-0144335.

PR 20-VW-1999) 9918-0144332.

PR 20-VW-1999) 9918-0144332.

PR 21-VW-1999) 9918-0144332.

PR 21-VW-1999) 9918-0144332.

PR 22-VW-1999) 9918-014524.

PR 22-VW-1999) 9918-014524.

PR 22-VW-1999) 9918-014524.

PR 22-VW-1999) 9918-014524.

PR 23-VW-1999) 9918-0145218.

PR 23-VW-1999) 9918-0145218.

PR 23-VW-1999) 9918-0145218.

PR 23-VW-1999) 9918-0145218.

PR 23-VW-1999) 9918-0145218.

PR 23-VW-1999) 9918-0145218.

PR 23-VW-1999) 9918-0145318.

PR 23-VW-1999) 9918-014431.

PR 23-VW-1999) 9918-014431.

PR 23-VW-1999) 9918-014431.

PR 23-VW-1999) 9918-014431.

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PR 23-VW-1999) 9918-014431.

PR 23-VW-1999) 9918-014431.

PR 23-VW-1999) 9918-014431.

PR 23-VW-1999) 9918-01431.

PR
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107
                                                                                                                                                                                                                                                                                          10 LDCIVRLEETHVQQQFDEGYEEGLVSGREDARHLGLKLGFFTGELIGFYRGCSALWNSAL 69
                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                            6 IDNVLNLEEBQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLS--
                                                                                                                                                                                                                                                                                                                64 HIDQYNNSSSLRNHLNNLEDIMAQISITNGDKEVEDYBKN------IKKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                       15.0%; Score 116; DB 21; Length 404; 26.0%; Pred. No. 0.0022; ive 22; Mismatches 51; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #28096.
                                                                                                                                                                                                                                                                                                                                                                                                                     ABG28105 standard; Protein; 237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
99US-0159329.
99US-0159330.
99US-0159637.
99US-0159638.
99US-0159584.
99US-0160767.
99US-0160767.
99US-0160767.
99US-0160767.
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99US-0160767.
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002 (first entry)
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.03
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73
N-PSDB; AAS92292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                      RNK 110
                                                                                                                                                                                                                                                                                                                                                                        RNK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                 14-0CT-1999
14-0CT-1999
18-0CT-1999
21-0CT-1999
21-0CT-1999
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                                                                                                                     22-0CT-1999)
22-0CT-1999)
25-0CT-1999)
25-0CT-1999)
26-0CT-1999)
26-0CT-1999)
26-0CT-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
ABG28105
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tage for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating insiders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human of the polypepticalication, but was obtained in electronic format directly from WIPO are fire into into the polypeptics.
                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                          Claim 20; SEQ ID No 58464; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AA;
                                                                                                         biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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71 SSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL 130
                                                                                                                                                     20
                                                              11 NLEEEQYELGFKEGOIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNN
12.9%; Score 99.5; DB 22; Length 237; 26.7%; Pred. No. 0.053; tive 23; Mismatches 46; Indels 19;
                                  Conservative
               Local Similarity
hes 32; Conserv
Query Match
                               Matches
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ABB11923 standard; peptide; 293 AA ABB11923;

(first entry) 11-JAN-2002 Human GK003 homologue, SEQ ID NO:2293.

Human, cytokine; cell proliferation, cell differentiation, growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; ofemotrasis, chemokinesis; thrombolysis, onogenesis, proliferation; metastesis; cancer; tumour, haematopoietic disorder; myelid cell disorder; lymphoid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; tissue respeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiantlammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic, osteopathic, vasotropic, cardiant, virucide, antibacterial, antifungal, vulnerary, antiulcer.

Homo sapiens.

130

70

221

WO200157188-A2

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Sequences ABA08225-ABA06230 represent 1300 moves internal polypeptides, and sequences ABA08225-ABA06230 represent nucleic acids encoding them. The invention also relates to vectors and recombinath host cells comprising a nuclectide of the invention, methods of detecting the nuclectides, antibodies against the polypeptides, methods of detecting the nuclectides of the invention. Although novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby cylving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; including cytokine, cell proliferation or cell differentiation activities; seem cell growth factor activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; tissue growth activity; immunomodulatory activity; activities; playeptides activities; chemotactic or chemokiner; activities; playeptides activities; chemotactic or chemokiner; activities; playeptides and nucleotides of thrombolypric activities; activities; polypeptides and nucleotides of conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., orteoporosis), and abnormal carefular growth. Polypeptides involved with tissue regeneration and vascular growth. Polypeptides encoding them) may be used to promote wound conditions in addition to immunochulatory activities may be used in the treatment of viral, bacterial infections in addition to immune disease with growth factor activity may be used to promote wound conditions and ulcers), while those with growth factor activity may be used in the treatment of viral, bacterial and fungal infections in addition to immune disease or accidental damage. The propeptides with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 SSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 NSTLINKINNLLDAVGQ------CEEY-----VLKHLKSITPPSHVVDLLDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 NLEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNN
                                                                                                                                                                                                                                                                                                      Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 99.5; DB 22; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 26.7%; Pred. No. 0.07 32; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 277; 1963pp; English.
                                                                                                                                                                                          Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide of the invention.
                                       05-FEB-2001; 2001WO-US03800.
                                                                               03-FEB-2000; 2000US-0496914.
                                                                                                                                                                                                                                                                                                                                                e.g. arthritis and cancer
                                                                                                                                                                                                                                       WPI; 2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293 AA;
                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                            N-PSDB; ABA09167
09-AUG-2001.
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Best Local S
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----VLKHLKSITPPSHVVDLLDSI 221

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Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptidet therapy; stem cell growth factor, haematopoiesis; tissue growth factor, immunomodulatory; cancer, leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, Drmanac RT, Asundi V, Zhou P,
Wang D, Wang J, Zhang J, Ren F, Chen
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in diagnosis and gene therapy -
                                                                 AAM78467 standard; Protein; 310
                                                                                                                                                                                                                                                                                                                                                   03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-UUN-2000; 2000US-0598075.
19-UUL-2000; 2000US-063325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653551.
20-OCT-2000; 2000US-0653325.
30-NOV-2000; 2000US-059325.
                                                                                                                                              Human protein SEQ ID NO 1129.
                                                                                                                                                                                                                                                                                                                            05-FEB-2001; 2001WO-US04098.
180 NSTLINKINNLLDAVGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAK51600
                                                                                                                                                                                                                                                                        WO200157190-A2
                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                     06-NOV-2001
                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                            AAM78467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xue AJ,
                                                                              The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALCHARTON OF SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Cac Y,
Wang ZW;
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κ,
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Wang D, Wang J, Zhang J, Ren F, Chen
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.9%; Score 99.5; DB 26.7%; Pred. No. 0.07; ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 251-252; 6221pp; English.
                             AAM79451 standard; Protein; 293 AA
                                                                                                                                                                                                                                                                                                                            27-APR-2000; 2000US-0560875.
20-UUN-2000; 2000US-0598075.
19-UUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0654561.
20-OCT-2000; 2000US-063325.
                                                                                                           Human protein SEQ ID NO 3097.
                                                                                                                                                                                                                                                                                                                2000US-0496914.
                                                                                                                                                                                                                                                                                      05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.74
These 32; Conservative
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAK52584
                                                                                                                                                                                                                                  WO200157190-A2.
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                  03-FEB-2000;
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                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
Zhao QA,
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                                                     AAM79451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xue AJ,
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Xu C, Cao Y, R, Wang ZW;

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
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                                                                                                                                                                                                                                                                                                                                         treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                           Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 NLEEEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.9%; Score 99.5; DB 22;
26.7%; Pred. No. 0.076;
tive 23; Mismatches 46;
Claim 20; Page 3362-3363; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
Les 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 AA;
                                                                                                                                                                                                                                                                                                                                                                             inflammation.
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Matches
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Gaps

19;

46; Indels

SSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL 130

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11 NLEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNN 70

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121 NMORRVKE-GYRDGIDAGKAVTLOOGFNOGYKKGABVILNYGRLRGTLSALLSWCHLHNN

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(first entry)

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                    Drosophila, developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 30363; 21pp + Sequence Listing; English
                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 30363
ABB67857 standard; Protein; 141 AA.
                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABL11960
                                                                                                                                                                                   WO200171042-A2
                                                        26-MAR-2002
                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                                                                                                                                                                                                               Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                           ABB67857;
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ABP6901
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XXAXAXAX
            71 SSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL 130
                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                              expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GYRDGIDAGKAVTLOQGFNOGYKKGAEVILNYGRLKGTLSALLSWCHLHNNNSTLINKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 GFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNNSSSLRNHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.8%; Score 99; DB 21; Length 107;
Best Local Similarity 27.0%; Pred. No. 0.021;
Matches 30; Conservative 21; Mismatches 42; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 NLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VLXHLKSITPXSHVVDLLDSI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                             Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; SEQ ID 6047; 71pp + CD-ROM; English.
                                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 6047.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                          gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NLLDAVGQ------CEEY--
                                                                                                          AAG01966 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-500381/45.
N-PSDB; AAC01972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
                                                                                                                                                                    06-OCT-2000
                                                                                                                                       AAG01966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                            RESULT
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Myers EW;

Li PWD,

Adams M,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDIVLTEEKEARLGYEE----GLKDGQEQGNEEGYKLGYAQGVSLG--EELGKI-LGQVV 65
                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; genome mapping; gene therapy; food supplement; virus; fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- DOYNNSSSLRNHIANLEDIMAQISITNGDK-EVEDYEKNIKKARNKIR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQQQLKHTDKVRRSLEQLRSLIEEFPRTNDPQADIVGAVQDIRSSHRRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 95.5; DB 22; Length 25.5%; Pred. No. 0.068; cive 29; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 1060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP69013 standard; Protein; 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.5
Matches 28, Conservative
                                                                                                                                                                                                                                                                 (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AA;
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RESULT 10 ABB67857

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The invention relates to an isolated polynuclectide (I) comprising a nuclectide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynuclectides are useful coding protein or complementary sequences. The polynuclectides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP68849) are useful as molecular weight markers, as food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzhaimer's disease), autojimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, indigal, parasitic), arthritis, etc.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO. At the wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626 GALOGKVEEDLELLDKSFETLADOTEWOSSHLFKYFQEVVQLWEAHOSELLVQELELEKR 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; nootropic; neuropricetive;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ren F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 GOLQGTKDQYLEGKEYGY----QTGFQRFLIIGYIQELMKFWLSH-------
                                                                                                                                                                                                                                                                                                                                                                                                              Zhao QA, F
Ghosh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides comprising sequences assembled from expres sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, o platelet or coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 95; DB 23; Length 1646; 25.2%; Pred. No. 2.1; rive 27; Mismatches 40; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; SEQ ID NO 1060; 1012pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Goodrich RW, Asundi V, Zhang J, Z
Ma Y, Yamazaki V, Chen R, Wang Z,
, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVIASITKETWKIDSLDNLVKEV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-2002; 2002WO-US05095.
                                                                                                                                                                                                                                                                                                                             05-MAR-2001; 2001US-0799451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               ΑÃ
                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Zhou P, G
Kue AJ, Yang Y, Ma
Wehrman T, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-759812/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1646 AA;
                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABZ11230
                                                                                                                                                                                                      WO200270539-A2.
                                                                                                    haemostatic; v
antiarthritic.
                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                               12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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The present invention relates to a new gene expression cassette comprising a secretory leader sequence encoding a signal peptide from clostridium difficile or signal peptides of analogous exported clostridium difficile or signal peptides of analogous exported clostridium difficile or signal peptides of analogous exported states and/or secreting them into the surroundings of the expression cassette is useful for presenting polypeptides on the surface of bacterial cells, and/or secreting them into the surroundings of the cells, for mucosal immunisation, induction of immunological tolerance and anti-tunour therapy in humans and animals, as vaccines, and for the treatment of prevention of fibrinolysis in arterial or venous occlusion and/or revitalising gangrenous or necrotic tissue in various diseases. The gene expression cassette may also be used to produce in the gut, e.g. peptides and enzymes for therapy and prophylaxis of various diseases; single, fusion or multiple polypeptide antigens of microbial, animal or mammalian or manmalian or manmalian or manmalian or injun for neonatal immune balanching, vaccination and carrier molecules separated or fused to the antigen to amplify or modulate immune response. Spores produced by calculations, e.g. Clostridium difficile are useful for both industrial production of vaccines and for local production of the desired polypeptides at the body sites desired. AAU12017-AAU12048 represent C. difficile S-layer protein cell wall binding portions end or C. ORF1, ORF2, ORF9, ORFE, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, ORF9, 
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                                                                                                                                                                                            anti-tumour therapy;
protein; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 KEGQIQGTKDQYL-----EGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNN 70
                                                                                                                                            Clostridium difficile S-layer protein cell wall binding portion (ORF7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 KEIKRLGAKDIYLIGGTAVLNKDIENKLKGNGLNVER-------INGKNRYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New gene expression cassette comprising a secretory leader sequence encoding a signal peptide from Clostridium difficile, useful e.g. for presenting polypeptides on bacterial cell surface, or as anti-tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
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                                                                                                                                                                                         Gene expression cassette; secretory leader sequence; anti-tucclostridial N-acetylmuramoyl-L-alanine amidase-like protein; fibrinolysis; gangremous tissue; necrotic tissue; infection; f-layer protein call wall binding portion; ORF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burman LG, Akerlund T, Mukherjee K, Katagihallimath N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 77-79; 113pp; English.
AAU12041 standard; Protein; 525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMIT-) SMITTSKYDDSINSTITUTET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2001; 2001SE-0101479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2001; 2001WO-SE01280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2000; 2000SE-0002139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 24.3.
Thes 34; Conservative
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                        Clostridium difficile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-122121/16.
                                                                                                                                                                                                                                                                                                                                                                        WO200194599-A1
                                                                                               09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-2001.
                                                  AAU12041;
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RESULT 12 AAU12041

151 RIHMLERHAREQETKLETTLQALE 174

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signaling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pot_sequences.
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 DNVLNLEBEQYELGFKEGQIQGTK--DQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSH
                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, SEQ ID NO 32421; 21pp + Sequence Listing, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 90; DB 22; Length 475; 25.7%; Pred. No. 1.3; ive 32; Mismatches 51; Indels
                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 32421
                                                                                                                                                     ABB68543 standard; Protein; 475 AA
                                            130 LVKE-----VGGTLQVS 141
                                                                         198 FIRDEKVIKAYVIGGTNSVS 217
                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0614150
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.7%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL12646
                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2.
                                                                                                                                                                                                                                                                                        pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions
                                                                                                                                                                                                             26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                   ABB68543
ID ABB
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The present invention relates to a new gene expression cassette comprising a secretory leader sequence encoding a signal peptide from Clostridium difficile or signal peptides of analogous exported clostridial N-acetylmuramoyl-L-alanine amidase-like proteins, linked clostridial N-acetylmuramoyl-L-alanine amidase-like proteins, linked comprises on cassette is useful for presenting polypeptides on the surface of bacterial cells, and/or secreting them into the surroundings of the cells, for mucosal immunisation, induction of immunological tolerance and anti-tunmour therapy in humans and animals, as vaccines, and for the treatment of prevention of fibrinolysis in arterial or venous occlusion and/or revitalising gangrenous or necrotic tissue in various diseases. The gene expression cassettem may also be used to produce in the gut, e.g. peptides and enzymes for therapy and prophylaxis of various diseases; single, fusion or multiple polypeptide antigens of microbial, animal or mammalian origin for neonatal immune balancing, vaccination animal or mammalian origin for neonatal immune balancing, vaccination animal or mammalian origin for neonatal immune balancing, vaccination animal or manimulate immune response. Spores produced by animal or manimulate immune response. Spores produced by clostridia, e.g. clostridia, e.g. clostridia, e.g. clostridia, e.g. clostridia, e.g. clostridia, e.g. clostridia, e.g. clostridia, e.g. complete and for local production of the desired polypeptides at the body sites desired. AMU12017-AMU12048 represent c.g. chifficile S-layer protein cell wall binding portions encoded by corpus respectively. The DNAs encoding these portions may be used in a respectively. The DNAs encoding these portions may be used in a cappane or the present invention.
                                                                                                                                                                                Gene expression cassette; secretory leader sequence; anti-tumour therapy; clostridial N-acetylmuramoy1-b-alamine amidase-like protein; cytostatic; fibrinolysis; gangrenous tissue; necrotic tissue; infection; S-layer protein cell wall binding portion; ORF6.
                                                                                                                                   Clostridium difficile S-layer protein cell wall binding portion (ORF6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New gene expression cassette comprising a secretory leader sequence encoding a signal peptide from Clostridium difficile, useful e.g. for presenting polypeptides on bacterial cell surface, or as anti-tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 75-77; 113pp; English.
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AAU12040 standard; Protein; 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIT-) SMITTSKYDDSINSTITUTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2000; 2000SE-0002139.
26-APR-2001; 2001SE-0101479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2001; 2001WO-SE01280.
                                                                                          (first entry)
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Best Local Similarity 27.5'
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                      Clostridium difficile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-122121/16.
                                                                                                                                                                                                                                                                                                                                                      WO200194599-A1.
                                                                                          09-APR-2002
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65 IDQYN-NSSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKAR-NKLRVIASITKETW 122

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                                                                                                                          570 ELQRIGIKKVYLIGGENSLSKOVQTQLSNMGISVER----ISGSDRYKTSISLAQKLNSI 625
                                                                                       EDIMAQISITNGDKEVED-YEKNIKKARNKLRVIASITKETWKIDSLDNLVKE---- 133
23 EGGIOGTKDOYLEGKEYGYOTGFORFLI-IGYIQELMKFWLSHIDQYNNSSSLRNHLNNL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Borrelia burgdorferi nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigenic protein; vaccine; Lyme disease; infection; detection.
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23.5%; Pred. No. 1;
.ive 32; Mismatches 47; Indels

 B. burgdorferi antigenic protein, t02A.aa BB002.

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97US-0050359.
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97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi
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N-PSDB; AAX61834.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 6062, Ap	Sequence 10, Appl	Sequence 10, Appl	Sequence 2884, Ap	Seguence 2, Appli	Sequence 53, Appl	Sequence 51, Appl	Sequence 1, Appli	Sequence 460, App	Sequence 299, App	Sequence 2331, Ap	Sequence 3400, Ap	Sequence 1646, Ap	Sequence 2, Appli	Sequence 5785, Ap
SUMMARIES	QI	US-10-032-585-6062	US-10-056-405-10	US-10-094-240-10	US-10-032-585-2884	US-10-312-841-2	US-10-240-453-53	US-10-239-676-51	US-10-178-194-1	US-10-311-455-460	US-10-311-455-299	US-10-311-455-2331	US-09-960-352-3400	US-10-311-455-1646	US-10-312-841-2	US-09-960-352-5785
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          Sequence 6062, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Torry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6062
LENGTH: 447
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Best Local Similarity 99.33
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Publication No. US20030166013A1
GENERAL INFORMATION
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TGGTTATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAAT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGAAAACCCCGATGATATGTGGTGA 447
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Matches 196; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Anopheles gambiae
US-10-056-405-10
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US-10-056-405-10/c
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US-10-032-585-2884/c

US-10-032-585-2884/c

Sequence 2884, Application US/10032585

Sequence 2884, Application Wo. US20030180953A1

GENERAL INFORMATION:

APPLICANT: Bo, Jian Boone

APPLICANT: Charles, Boone

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey

TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

FILE REFERENCE: 10182-005-999

CURRENT APPLICANTION NUMBER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2884

LENGTH: 65
RESULT 3
US-10-094-240-10/c
is Sequence 10, Application US/10094240
is Sequence 10, Application US/10094240
is Publication No. US2030082637A1
is GENERAL INFORMATION:
is TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
is TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
is CURRENT FILING DATE: 2001-03-08
is PRIOR PILING DATE: 2002-01-24
is PRIOR FILING DATE: 2001-01-26
is NUMBER OF SEQ ID NOS: 27
is SEQ ID NO 10
is SEQ ID NO 10
is ERGCTH, 4985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4985;
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Pred. No. 0.0073;
0; Mismatches 181; Indels
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Best Local Similarity 51.0%;
Matches 196; Conservative
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APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Diagnosis of Diseases Associated
TITLE OF INVENTION: Diagnosis of Diseases Associated
TITLE OF INVENTION: With DNA TRANSCRIPTION
TITLE OF INVENTION: With DNA TRANSCRIPTION
FILE REPERENCE: 5013-1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT APPLICATION NUMBER: DCT/EPO1/03973
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
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APPLICANT: PIEBENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ITATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTG
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Pred. No. 0.19;
0; Mismatches 199; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 47.8%;
Matches 182; Conservative
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US-10-239-676-51/c
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US-10-312-841-2
US-10-312-841-2
Publication No. US20030186277A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT PELING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 TIGGITALCCCATALAGAICAATATAATAACICTTCTTCACTTCGGAATCATTTGAATAA 239
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                                                                                                                                                               Query Match
14.4%; Score 64.2; DB 13; Length 3673778;
Best Local Similarity 54.2%; Pred. No. 0.57;
Matches 173; Conservative 0; Mismatches 143; Indels 3; G
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                           Length 65;
                                                                                                                     0; Indels
                                                                    Query Match
14.5%; Score 65; DB 13;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 65; Conservative 0; Mismatches 0
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Publication No. US20030148326A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
  ; ORGANISM: Candida albicans
US-10-032-585-2884
                                                                                                                                                                                                                                                         64 AAAGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (379615)
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US-10-178-194-1
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US-10-239-676-51
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                                                                                                                                                                                                                                                                                                Length 9539;
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Pred. No. 0.19;
0; Mismatches 199;
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APPLICANT: Jeffrey Gulcher
TITLE OF INVANTION: HUMAN NARCOLEPSY GENE
FILE REPERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/10/178,194
CURRENT FILING DATE: 2002-06-21
PRIOR PEPLICATION NUMBER: US/09/426,290
PRIOR FILING DATE: 1999-10-25
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 168575
NT FILING DATE: 2002-09-24
APPLICATION NUMBER: PCT/EP01/03968
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Publication No. US20030166904A1
                                                                                                                                                                                                                                                                                                14.0%;
47.8%;
                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                     PRIOR FILING DATE: 2001-04-06
2000-04-06
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.8
Matches 182; Conservative
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SEQ ID NO 51
LENGTH: 9539
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ORGANISM: Homo Sapiens
FEATURE:
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                          DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Disgonsis of Diseases Associated with the Immune System by Deter
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: 105/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
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0; Mismatches 218; Indels
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Publication No. US20030143606A1
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APPLICANT: PIEPENBROCK, Christian
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Best Local Similarity 48.1%;
Matches 203; Conservative
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APPLICANT: DLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BEREIN, Kur.
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
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Pred. No. 0.52;
0; Mismatches 227; Indels
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Pred. No. 0.63;
                 ; FEATURE:
; NAME/KEY: unsure
; LOCATION: 214, 2796..2797, 4347
; OTHER INFORMATION: n is a or g or c or
US-10-311-455-299
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Publication No. US20030143606A1
GENERAL INFORMATION:
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Best Local Similarity 46.3%;
Matches 196; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: DIEK, Alexander
APPLICANT: DIEK, Alexander
APPLICANT: DIEKENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
FILE OF INVENTION: Cytosine methylation
FILE REPRENCE: 50.31.014
FILE REPRENCE: 50.31.014
CURRENT APPLICATION NUMBER: US/10/311,455
FRICK APPLICATION NUMBER: DE 10032529.7
FRICK PILING DATE: 2000-07-02
FRICK FILING DATE: 2000-07-03
FRICK FILING DATE: 2000-09-01
FRICK FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
STONMAR: 6100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 CTGGATTTCAACGATTTTTAATCATTGGTTATTTCAAGAATTAATGAAATTTTGGTTAT 187
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60.2; DB 13; Length
Pred. No. 0.59;
0; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: chemically treated genomic DNA US-10-311-455-460
## PRIOR FILING DATE: 2001-07-02
| PRIOR APPLICATION NUMBER: DE 10032529.7
| PRIOR FILING DATE: 2000-06-30
| PRIOR FILING DATE: 2000-09-01
| NUMBER OF SEQ ID NOS: 2424
| ENDIRENCE FILING DATE: 2000-09-01
| SEQ ID NO 460
| LENGTH: 17183
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Publication No. US20030143606A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 49.9
Matches 185, Conservative
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US-10-311-455-299/c
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Associated with the Immune System by Deter
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                                                                                                                                                  AAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTG 365
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                                                                                                                                                                                    AGAAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCA
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                                                                        AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1646
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Pred. No. 0.8;
0; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                   Sequence 1646, Application US/10311455
Publication No. US20030143606A1
Publication No. US20030143606A1
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
TITLE OF INVENTION: Diagnosis of Diseases Ass
TITLE OF INVENTION: Oyosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
CURRENT FILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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Best Local Similarity 48.1%;
Matches 198; Conservative
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Patent No. US20020137139A1
GENERAL INFORMATION
APPLICANT: March, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE, AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10299)
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
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                                                                      AGAAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAAGAATATGGTTATCA
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 15-LIB3058-052-Q1-K1-D11
US-09-960-352-3400
227;
Mismatches
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Conservative
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196;
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                                                                                                                            FEATURE:
NAME/KEY: unsure
NAME/CATION: (76), (90)
OCHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1
US-09-960-352-5785
                                                                                                                                                                                                                                                                         Score 57.8; DB 10;
Pred. No. 0.56;
0; Mismatches 187;
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Best Local Similarity 47.6%;
Matches 170; Conservative
        CURRENT FILING DATE: 2001-(
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5785
LENGTH: 516
                                                                                         TYPE: DNA ORGANISM: Bos taurus
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                                                                                                                                                                                        APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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Patent No. US20020137139A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Neigbing
APPLICANT: Tao, Neigbing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.0066/37-21(10299)
CURRENT APPLICATION NUMBER: US/09/960,352
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                                         2844 AAACTAATTTCATTCAATAATATTAATTAATATCCACCTTATACTTAATA 2793
365 GGAAAATTGATTCATTGGATAATTTGGTGAAAGAAGTAGGTGGAACTTTACA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3673778;
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48.8%; Pred. No. 6.1;
tive 0; Mismatches 193;
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                                                                                                                                         ; Sequence 2, Application US/10312841; Publication No. US20030186277A1; GENERAL INFORMATION:
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LOCATION: (379615)
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US-09-960-352-5785/c
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LENGTH: 3673778
                                                                                                 RESULT 14
US-10-312-841-2/c
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269

Length 516; Indels

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109084 ТСТАААТЫТЫТЫТЫТЫТТЫТТЫТТЫТЫЙТЫТЫТЫМТЫ ТОТААТЫТЫТЫТЫТЫТЫ 109143
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21, Appli
15, Appl
47, Appl
31, Appli
73, Appli
                                           150, App
41, Appl
41, Appl
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                                                                                                                                                              Sequence 47, P
Sequence 1, P
Sequence 13, P
Sequence 7, Ap
Sequence 2, Ap
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        Sequence
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13.7%; Score 61.2; DB 4; Length 10
Best Local Similarity 48.1%; Pred. No. 0.00042;
Matches 203; Conservative 0; Mismatches 218; Indels
US-07-991-867B-1
US-08-544-332-1
US-09-370-861A-1
US-09-134-001C-150
US-09-370-861A-41
US-09-370-861A-74
US-09-370-861A-74
US-09-004-83B-70
US-09-0134-001C-2120
US-09-134-001C-2120
US-09-134-001C-2120
US-09-134-001C-2120
US-09-134-001C-2120
US-09-134-001C-2120
US-09-134-001C-2120
US-09-134-001C-2120
US-09-134-001C-2120
US-09-136-100-13
US-08-764-100-13
                                                                                                                                                                                                                                                                                                                               Sequence 1. Application US/09426290
Patent No. 6410712
GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafedottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUVAN NACOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 1
                                                                                                                                                                                                                                                                     ALIGNMENTS
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    LENGTH: 168575
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LOCATION: (211:
NAME/KEY: CDS
LOCATION: (952:
NAME/KEY: CDS
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NAME/KEY: CDS
LOCATION: (110
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LOCATION: (12)
    JS-09-426-290-1
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Sequence 186, App
Sequence 13, Appl
Sequence 13, Appli
Sequence 21, Appli
Sequence 218, Appl
Sequence 2137, Appli
Sequence 1, Appli
Sequence 1, Appli
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                                                                                      February 16, 2004, 10:57:21 ; Search time 64 Seconds (without alignments) 3082.785 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgnZ_6/ptodata/2/ina/5A_COMB.seq:*
/cgnZ_6/ptodata/2/ina/5B_COMB.seq:*
/cgnZ_6/ptodata/2/ina/6A_COMB.seq:*
/cgnZ_6/ptodata/2/ina/6B_COMB.seq:*
/cgnZ_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgnZ_6/ptodata/2/ina/PCTUS_COMB.seq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-901-861-3

US-08-901-861-3

US-08-901-861-3

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US-09-306-593-1
PCT-US93-07261-10
US-08-545-528D-1
US-08-107-755A-1
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                                                                                                                                                                                                                                   569978 seqs, 220691566 residues
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                                                           OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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186 ATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGA 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 AAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTG 365
                                   SEQUENCES OF ASHBYA GOSSYPII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 GAAAATTGATTCATTGGATAATTTGGTGAAGAAG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Stainer, Sabine
APPLICANT: Mendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUEN
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 186, Application US/08998416
Patent No. 6239264
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/
TELECOMMUNICATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORRESPONDENCE ADDRESS:
SORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: SIEM PC compatible
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CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 435
FILING DATE:
CLASSIFICATION: 435
FRICK APPLICATION: 435
FRICK APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENTY SLEPHEN A.
REGISTRATION NUMBER: 29,768
RECERRENCE/DOCKET NUMBER: 30472/114 IMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463 Patent No. 5670367
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INPORMATION FOR EBQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-232-463-14
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IMMEDIATE SOURCE
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29,655
FP: NIH121.001CP1
                                  REFERENCE DOCKET NUMBER: NIHI.
TELECOMUNICATION INCORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                     12.4%;
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Best Local Similarity 49.3
Matches 178; Conservative
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Matches 185; Conserv
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HATI-SENSE: NO
US-08-487-826B-13
                                                                                                                                                                          TOPOLOGY: lin
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US-09-801-861-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-801-861-3/c
                                                                                                                                                                                                                                                                     Query Match
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APPLICANT: Sim, Kim L.
APPLICANT: Sim, Kim L.
APPLICANT: Miller, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS NUMBER OF SEGUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               68 AAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCAAA 127
                                                                                                                                                                                                                                                                                                 484
                                                                                                                                                                                                                                                                                                                                187
                                                                                                                                                                                                                                                                                                                                                                                                                  188 CCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 ATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308 ATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 rihitgarahrerarrahahrarriharrahagaaharahahahrahahahrarrah 244
                                                                                                                                                                                                                                                                                                                           128 CTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGTTAT
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                           ;
0
                                                                                                                                            Length 615;
                                                                                                                                                                      0; Mismatches 197; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                          8; DB 3;
0.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 620 Wewport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                          Score 55.8;
Pred. No. 0.
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APPLICATION NUMBER: US/08/487,826B
FILLING DATE: 10-SEP-1993
CLASSIFTCATION: 435
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Patent No. 5993827
                                            linear
s: DNA (genomic)
                                                                                                                                          12.5%;
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LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                      Best Local Similarity 46.9
Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 TAACTAATTTA 233
                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (9¢
) ORIGINAL SOURCE:
US-08-998-416-186
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                                                                                                                                         Query Match
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15815
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Patent No. 6492154
GENERAL INFORMATION:
ATIONAT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: TAREBORE
FILE REFERENCE: CLO01098
CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 AAATATTAAAAAGGCAAGAAATTAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTG 365
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                                                                                                                                                                                                                                                                                                                                15756 AAAAAAATTAAAAATGTTAAAAAAAAAAATATATACATAAAATAAAAAAATTTATTT
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                                                                                          9 TATAGATATAGATAATGTATTAAATTTAGAAGAAGAACAATATGAATTAGGATTTAAAGA
                                                                                                                                                                                                                                                                                   126 AACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGTT
                                                  Gaps
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Score 55.6; DB 2; Length 19124; Pred. No. 0.0046;
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                                          0; Mismatches 174; Indels
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Pred. No. 0.008;
0; Mismatches 174;
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18271
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                                                                                                                                                                                                                                                                                                                                                                                              18212 TTATTGTATTATTATTAATTTATTATTAATAGGAAACTATATAATAATATTGTATTATAAATA 18153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18152 ATTÍTTÁTÁTÁTGÁGATTÁTATÁTTTTTTTTTCGCTCGGÁTTATTCAGÁÁTTÁGAGTAÁCAA 18093
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                                                                                                                                                                                                                              18330 TGTTGATATGTAGAATTACTTTATGTTTTTGTTTGATAAAAGAATTAAGAAATTAAAAA
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APPLICANT: Greiner, Beate
APPLICANT: Unger, Eberhard
APPLICANT: Gother, Gislinde
APPLICANT: Gother, Gislinde
APPLICANT: Schwerdel, Marc
TITLE OF INVENTION: EXPRESSION
FITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 0.2401.1678
CURRENT APPLICATION NUMBER: US/09/627,122
NUMBER OF SEQ ID NOS: 2.3
SOFTWARE: Patentin Ver. 2.1
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                                                                                                    Length 19124;
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                                                                                                 Score 54.4; DB 2;
Pred. No. 0.008;
0; Mismatches 186;
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Patent No. 6472521
PERERL INFORMATION:
APPLICANT: Unlmann, Eugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17973 GATATATATATTAGAAAA 17956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-627-122-21
                                                                                                      12.2%;
50.0%;
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Best Local Similarity 47.7%;
Matches 157; Conservative
                                                                                                    Query Match
Best Local Similarity, 50.0
Matches 189; Conservative
                                        , ANTI-SENSE: NO
US-08-487-826B-13
MOLECULE TYPE:
HYPOTHETICAL:
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LENGTH: 5340
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Parent No. 5993827
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Miller, Louish
APPLICANT: Miller, Louish
APPLICANT: Percerson, David S.
APPLICANT: Wellems T.
TITLE OF INVENTION: BINDING DOWAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
                                                       31505 татататалалатататалалан жанататалан жанататалалан татататалалалан жана 31455
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                                                                                                                                            196 GATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAGATATTATG
                    16 ATAGATAATGTATTAAATTTTAGAAGAAGAACAATATGAATTAGGATTTAAAGAAGGTCAA
                                                                                                    76 ATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCAAACTGGATTT
                                                                                                                                                                                      CAACGATTTTTAATCATTGGTTATTCAAGAATTAATGAAATTTTGGTTATCCCATATA
                                                                                                                                                                                                                                                                                                                                                      ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORTWARE: PatentIn Release #1.0, Version #1.25
SOUTHWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-52P-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor STATE: California
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REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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69 AGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCAAAC 128
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                                                                                                                                                 541 TAAATAAATAAAATGAAATATAATTTAAATAATAATAAAAATTA-ATAATAAGAAATT 483
                                                                                                                                                                                                                                               482 AAAGTTAAATTTAATTTTAATAATAATTCTTATAAAAGATTAAATAATAATAATCAACA 423
                                                                                                                                                                                                                                                                                                189 CCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAGA 248
                                                                                                                                                                                                                                                                                                                                           422 TAATATTTATAAAATAGATATTATAATAAAATAATAATTTACAATATTTAAATAATT 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 TATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGGAA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                       302 TATTGATAATCTATTTAATAATTAAAGAAAATAATAATATCTAATAATATTTTAAT 243
       9 TATAGATATAGATAATGTATTAAAATTTAGAAGAAGAACAATATGAATTAGGATTTAAAGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCES OF ASHBYA GOSSYPII
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATER: PRESEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: No. 6239264artis Corporation
STREET: 3064 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Dhlippe
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUEN
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: 919-541-8587
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                                             1833 ATATGATAAGTCAAAAAAAATTATAAATCTGTTTTTATGAATTCTGTAAAAAGATAGA 1774
126 AACTGGATTTCAACGATTTTTAATCATTGGTTATTTCAAGAATTAATGAAATTTTGGTT 185
                                                                                                                                                                                            246 AGATATTATGGCACAAAATTTCTATAACGAATGGAGATAAAGGAAGTTGAAGATTATGAAAA 305
                                                                                           186 ATCCCATATAGATCAATATAAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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Pred. No. 0.015;
0; Mismatches 191; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: 24-DEC 1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/98/98,416
FILING DATE: 13-DEC 1996
ATTONNEY/AGENT INPORMATION:
NAME: MASIGN JUMBER: 38,241
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 919.541-95807
                                                                                                                                                                                                                                                                                                                                   1713 TAATAATGATATTAAAAGGAAGATAACAA 1685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 288, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Mohr, Christine APPLICANT: Wendland, Jurgen APPLICANT: Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 48.1%;
Matches 178; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAG1241RP
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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US-08-998-416-288
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Matches 138; Conservative
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Sequence 3, Application US/08213419B
Patent No. 6333406
GENERAL INFORMATION:
APPLICANT: Inselburg, J. et al.
TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
FILE REPERENCE: JII-002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR PAPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1922-04-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 6124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGG 366
                                                                                                                                                                                                                                                   68 AAGGTCAAATACAAGGAACAAAGATCAATATTTAGAAGGAAAGAATATGGTTATCAAA 127
                                                                                                                                                                                                                                                                                                                       128 CTGGA-TITCAACGATTITIAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGTTA 186
                                                                                                                                                                                                                                                                                                                                                                                            484 ITTAAAGITTAAATTAATTITIAATAATTATTOITATAAAAAGATTAAATAATAATAAATCAA 425
                                                                                                                                                                                                                                                                                                                                                                                                                              187 ICCCATATAGATCAATATAACACTTCTTCACTTCGGAATCATTTGAATAATTTGGAA 246
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Pred. No. 0.06;
                                                                                                                                               Length 636;
                                                                                                                                           Score 51.2; DB 3; Length 6 Pred. No. 0.025; 0; Mismatches 193; Indels
; TYPE: nucleic acid
; STRANDEDNES: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORTGINEAL SOURCE:
; ORGANISM: PAGI692RP
US-08-998-416-1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%;
                                                                                                                                             Query Match
Best Local Similarity 47.8%;
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 AAAATTGATTCA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 ÁTÁÁCTAÁTTTÁ 233
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NAME/KEY: CDS
LOCATION: (3580)...(3720)
NAME/KEY: CDS
LOCATION: (3850)...(5835)
S-08-213-4198-3
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CDS
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Best Local Similarity
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US-08-213-419B-3
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Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoci
Patent No. 6503729
TILLE OF INVENTION: januaschii
FILE REPERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT PILING DATE: 1997-080-22
PRIOR PATICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
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                                                                                                1563 ACGCATACACATTIGICATTATTITITITAGGIGTTATATTIAACAAAAAIGITA 2622
                                                                                                                                                                                                                                                                                                                                                                                                   2623 TAAAATGTACAGGAGAAAGTCAAACAGGTAATACAGGAGGAGGTCAAGCAGGTAATACAG 2682
                                                                                                                                                    184
                                                                                                                                                                                                                                                     185 TATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGG 244
                                                                                                                                                                                                                                                                                                                                                      245 AAGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAA 304
                                                                                                                                                                                                 125 AAACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGT
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2683 TAGGAGATCAAGCAGGTACTACAGGAGGAAGTCCACAAGGTAGTA 2727
                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 AAAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTA 349
0; Mismatches 147; Indels
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (28222)...(28222)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (98159)..(98
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LOCATION: (28257)..(28
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S E	TION: (103998)(c_feature 3948)(1 770%.p.e	KEY: misc feature ION: (163385)(16338	information: n equal KEY: misc feature ION: (191989)(19198	INFORMATION: n eq KEY: misc feature	FION: (191995)(: misc_feature : (231980)(2	KEY: misc feature ION: (234187)(23418	INFORMATION: n equal KEY: misc feature	ION: (234220)(INFORMATION: n	NEI: MISC ION: (2348 INFORMATI	<pre>KEY: misc feature ION: (309398)(30939</pre>	INFORMATION: n eq	ION: (309418)(INFORMATION: n	KEY: misc feature ION: (312837)(31283	INFORMATION: n equal KEY: misc feature	ION: (312993)(INFORMATION: n	E CON I	misc feature (559167) (55916	INFORMATION: n equal	INFORMATI	misc_feature (600992)(60099	INFORMATION: n equa KEY: misc feature FON: (622708) (6227	INFORMATION: n equal	N: (657081) (657081)	INFORMATION: "Equals KEY: misc feature TON: (657703) (657203)	R INFORMATION: n equals	rion: (674435)(674435) R INFORMATION: n equals	KEY: misc feature ION: (682442)(682442)	R information: n equals / /KEY: misc feature	TION: (/13652)(/13652) TINFORMATION: n equals	NAME/KEI: WISC LEATURE LOCATION: (741684)(741684) OTHER INFORMATION: n equals	

844063 AGAAAAAGAAAAACCTAAAGAAGTAAAAAAAGGAGATTAAAAAAGAAACTGAAGAAAAT 844004 844003 AGAAAAAAAAAAAAAATITGITAAGAAAGAAGAAAAAGAACAATITATAAAAAAATC 843944 96 ATATITAGAAGGAAAAGAATATGGTTATCAAACTGGATTTCAACGATTTTAATCATTGG 155 36 AGAAGAAGAACAATATGAATTAGGATTTAAAGAAGGTCAAATACAAGGAACAAAAGATCA 0; Gaps Query Match 11.0%; Score 49; DB 4; Length 1664976; Best Local Similarity 45.5%; Pred. No. 0.15; Matches 175; Conservative 0; Mismatches 210; Indels 0; NAME/KEY: misc_feature

LOCATION: (875539)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (875539)..(871619)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1084830)..(1084830)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (11096846)..(1096846)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (11096846)..(11096846)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1130881)..(1313224)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1343943)..(1343941)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1343943)..(1343941)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1345941)..(1569020)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (14602912)..(1602912)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1602912)..(1602912)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1602912)..(1602912)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1602912)..(1603934)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1603998)..(1603998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1603998)..(1603998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1603998)..(1603998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1603998)..(1603998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1603998)..(1603998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1603998)..(1603998)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
LOCATION: (1603998)..(1603998)

OTHER INFORMATION: n equals a, t, c, or מ 占 LOCATION: (779455)...(779455) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature d ò 셤 216 TICACTICGGAATCATTIGAATAATTIGGAAGATATTAIGGCACAAATTICTATAACGAA 275

156 TIATATICAAGAATTAATGAAATTTTGGTTATCCCATATAGATCAATAATAACTCTTC 215

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Sequence 1, Application US/08446855A Patent No. 5849573 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                            Arlington
: Virginia
RY: USA
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APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: URBALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT FILING DATE: 2000-12-08
PRIOR PRILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
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   843823 TAĞTAGATAAAATGGATAĞCTAAAĞACATCGATGCCGTGATTGAGATATATGAAGATTC 843764
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                                                                                                                 336 AGTGATAGCTAGTATAACTAAAGAAACTTGGAAAATTGATTCATTGGATAATTTGGTGAA
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Pred. No. 0.11;
0; Mismatches 183; Indels 3
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; Sequence 70, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-70
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Best Local Similarity 47.9%;
Matches 171; Conservative
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RESULT 13 US-08-446-855A-1/C

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Best Local Similarity 46.0%; Pred. No. 0.14;
Matches 198; Conservative 0; Mismatches 230; Indels
                                                                                                                                                                                                           E: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
APPLICANT: O'SULIVON: William J
TITLE OF INVENTION: Nuclectide sequence encodi
TITLE OF INVENTION: phosphate syntherase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATCHILD RELEASE #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
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NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFRENCE/DOCKET NUMBER: 47-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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Best Local Simi
Matches 145;
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                                                                                                                                                                                          APPLICANT: Stewart et al.
ITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate Patent No. 618396
ITLE OF INVENTION: Synthetase II
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/150,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.7%; Score 48; DB 3; Length 8920;
Best Local Similarity 46.0%; Pred. No. 0.14;
Matches 198; Conservative 0; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER PILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER APPLICATION NUMBER: 04946,855
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1995-07-06
NUMBER: OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver: 2.0
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US-09-601-198-75/c
; Sequence 75, Application US/09601198
; Datent No. 6511583
; GENERAL INFORMATION:
                                                                                                                                      Sequence 1, Application US/09150741
Patent No. 6183996
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Plasmodium falciparum US-09-150-741-1
  428 ACCCCGATGA 437
                                     459 AACTATATTA 450
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APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Leffcwitz, Elliot
TITLE OF INVENTION: WILLELE ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/22
CURRENT PAPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 1996-01-20
PRIOR FILING DATE: 1996-01-30
NUMBER OF SEQ ID NOS: 181
SOFTRARE: PATENTIN VEr. 2.0
SEQ ID NO 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4482 ATTGGTGGCCAACAACAAAATTAATACTACATGTTTAAGGATGAATTCACTACTAAA 4423
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ne : 72 secs
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; ORGANISM: Ureaplasma urealyticum
US-09-601-198-75
Cassell, Gail H.
Chen, Ellson Y.
Glass, Jennifer S.
Glass, John I.
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ilarity 47.1%;
Conservative
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Sequence:

Title: Perfect :

Searched:

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                                             Candida albicans.
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Candida albicans e
Probe for DNA enco
Anopheles gambiae
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/SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT.
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT;*
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Database :

Result Ño.

AmEPV genome fragm Plasmodium falcipa

Bussey

Boone C,

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Identifying genes essential to fungal metabolisms and identifying potential therapeutic agents that target these genes -
                                                                                                     20-FEB-2001; 2001WO-US05551.
                                                                                                                               18-FEB-2000; 2000US-0183534.
                                                                                                                                                          (ELIT-) ELITRA PHARM INC
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                                                                                                                                                                                                                 WPI; 2001-489080/53.
P-PSDB; AAU15103.
                  Candida albicans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a Candida albicans protein. The present sequence encodes a Candida (1989) 10aDR527, 20aDR527, CaPLO24, CaNL260, and CaDR361. These genes are essential for survival, and so are good targets for antifungal agents. The Candida albicans genes and their derived proteins are used to screen compounds for the ability to inhibit the activity of the protein, i.e. for antifungal activity. The proteins are also used to generate a protein antibuday response against fungal infections in mammals. The Candida albicans proteins and their antibodies, are used for diagnosing fungal infections, specifically C. albicans (in standard amplification, hybridisation or immunological assays, and for studying
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                                        New polynucleotides from Candida albicans and their derived proteins, useful for diagnosis and treatment of fungal infections and for drug screening -
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100.0%; Score 447; DB 22; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.2e-70;
Matches 447; Conservative 0; Mismatches 0; Indels 0;
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WPI; 2001-050024/06
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                                                   The present invention relates to novel methods for constructing fungal strains useful for identification and validation of gene products as targets for therapeutic agents, for creating a collection of identified essential genes, and screening assays for the discovery of new drugs. The invention provides the GRACE (gene replacement and conditional expression) method for the construction of mutent organisms. Eferred to as GRACE strains of the organism. The invention can be applied to any organism, particularly a pathogenic fungus e.g. Candida albicans, aspergillus fungatus and Cryptococcus neoformans. The methods are useful to identify agents that may be used in the treatment of fungal infections. AAS23381-AAS2342 represent C. albicans essential genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TIGGAAATATITITGGCACAAATTICTATAACGAATGGAGATAAAGAAGTITGTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TGGTTATCCCATATAGATCAATATAACTCTTCTTCACTTCGGAATCATTTGAATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAAAAAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TATCAAACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 447 BP; 193 A; 38 C; 80 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 442.2; DB 2
Pred. No. 8.7e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.9%; Sco...
99.3%; Pred. No. e...
0; Mismatches
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Claim 22; Page 167; 324pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.3
Matches 444; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion or replacement by a cassette having an expression of the second allele by the terologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene the cells having both alleles modified are useful for identifying a gene that cells having both alleles modified are useful for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus to an antifungal agent that inhibits the growth of a diploid fungus contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus cand for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modilates the compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, cativity of inhibit growth or proliferation of C. albicans cells and for treatment in infection by C. albicans. The present sequence is that of an essential candida albicans gene used in the method of the invention. Note: The sequence data for this patent is not represented in the printed the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression
                                                                                                                                                                                                               Fungus, yeast, tetracyclin, promoter, GRACE strain, biosynthesis, signal transduction; DNA replication, cell division, growth, proliferation, Candida albicans, fungicide, antifungal, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.9%; Score 442.2; DB 24; Length 447; Best Local Similarity 99.3%; Pred. No. 8.7e-70; Matches 444; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 37; SEQ ID NO 6062; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 447 BP; 193 A; 38 C; 80 G; 136 T; 0 other;
                                                                                                                                                                       Candida albicans essential gene SEQ ID NO 6062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bussey H,
                                         ABZ31775 standard; DNA; 447 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-2000; 2000US-259128P.
20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2001; 2001WO-US49486.
                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-566694/60
P-PSDB; ABP73225.
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                                                                                                                                                                                                                                                                                                     Candida albicans,
                                                                                                                                                                                                                                                                                                                                               WO200253728-A2.
                                                                                                                                30-JAN-2003
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                                                                                   ABZ31775;
RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a probe for DNA encoding a Candida albicans protein. The specification describes genes CaDRA472, CaDR489, 1CaDR527, CaPL024, CaNL260, and CaDR361. These genes are essential for survival, and so are good targets for antifungal agents. The Candida albicans genes and their derived proteins are used to screen
TTTAAAGAAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAAAATATGGT
                                                                                                                                           121 TATCAAACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTT
                                                                                                                                                                                  181 TGGTTATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAAT
                                                                                                                                                                                                                  TGGTTATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAAT
                                                                                                                                                                                                                                                                                                                                                      301 GAAAAAAATTTAAAAGGCAAGAAATAAATTAAGAGTGATAGTTATAGTTATAACTAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                             361 ACTIGGAAAATTGATTCATTGGATAATTTGGTGAAAGAAGTAGGTGGAACTTTACAAGTT
                                                                                                                 TATCAAACTGGATTTTCAACGATTTTTAATCATTGGTTATTTTCAAGAATTAATGAAATTT
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                                              TTTAAAGAAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGT
                                                                                                                                                                                                                                                       TTGGAAGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTAT
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for drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides from Candida albicans and their derived useful for diagnosis and treatment of fungal infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe for DNA encoding a Candida albicans protein CaNL260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC86756 standard; DNA; 326
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                                                                                                                                                                                                                                                                                                                                                            ATTICAACGAITITITAATCAITGGITATATICAAGAATTAATGAAATTITGGITATCCCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAAAAATAT 311
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compounds for the ability to inhibit the activity of the protein, i.e. for antifungal activity. The proteins are also used to generate a protective antibody response against fungal infections in mammals. The Candida albicans proteins and genes, and their antibodies, are used for diagnosing fungal infections, specifically C. albicans (in standard amplification, hybridisation or immunological assays, and for studying pathogenic fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mosquito olfaction polypeptides and polynucleotides, useful for mosquito management, i.e. controlling the pest and disease vectors, or for identifying pest control agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae; mosquito; olfactory gene; arrestin 1; pest control; odourant receptor; olfaction; gene; ds.
                                                                                                                                                                                                                                        AGATATAGATAATGTATTAAATTTAGAAGAAGATCAATATGAATTAGGATTTAAAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                      TATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAGATAT
                                                                                                                                                                                                           12 AGATATAGATAATGTATTAAATTTAGAAGAAGAACAATATGAATTAAGGATTTAAAGAAGG
                                                                                                                                                                                                                                                                     TCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCAAACTGG
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                                                                                                                                                  DB 22; Length 326;
                                                                                                                                       Sequence 326 BP; 146 A; 27 C; 53 G; 100 T; 0 other;
                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAAAAGGCAAGAAATAAATTAAGAG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 TAAAAGGCAAGAAATAAATTAAGAG 326
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ABQ75107 standard; cDNA; 4985
                                                                                                                                                  72.6%;
99.7%;
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2002US-0056405.
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                                                                                                                                                                Best Local Similarity ... Matches 325; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-627421/67.
                                                                                                                                                Query Match
Best Local Similarity
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The present invention describes a purified Anopheles gambiae olfaction polypeptide comprising a 383, 394, 380, 411, 412, 391, 157 or 401 residue amino acid sequence (see ABP52831 to ABP52840) ($11), a conservatively modified amino acid sequence of them, or a sequence of ($11) with at less to comprising; (a) a nucleotide sequence encoding the purified Anopheles gambiae olfaction polypeptide; or (b) a nucleotide sequence that of phyridises under stringent conditions to a hybridisation probe comprising (a) spiritied Anopheles of hybridises under stringent conditions to a hybridisation probe comprising a 1964, 1129, 1142, 1136, 1194, 1176, 474 or 1206 nucleotide sequence (see ABQ75102 to ABQ75102 and ABQ75110 to ABQ75113) ($2), or its complement; and ($2) a method for identifying an agent that binds to mosquito olfaction molecules comprising; (a) providing an isolated mosquito olfaction molecule; (b) contacting a test agent with the isolated mosquito olfaction molecule; and (c) detecting specific binding comprising the test agent to the isolated mosquito olfaction in molecules are useful for mosquito olfaction binding identifies the test agent as a mosquito of the test agent to the isolated mosquito olfaction molecules are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2678
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                                                                                                                                                                                                                                                                                                                                                                                                            for mosquito management, i.e. controlling this pest and disease vector. A method from the present invention of screening for substances that modulate arrestin-dourant receptor interaction is useful for identifying pest control agents. The present sequence represents Anopheles gambiae dourant receptor 2 genomic DNA from the present invention.

N.B. The features given in figure 4a are tentative and do not directly encode SEQ ID NO:6 (ABP52035)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAACTGGATTTCAACGATTTTTAATCATTGGTTATTATTCAAGAATTAATGAAATTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2730 AATAATGTATAATGAATAACAATA-----ATAATAATAATAATAATAATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch al Similarity 51.0%; Pred, No. 0.00057, 196; Conservative 0; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4985 BP; 1319 A; 1058 C; 990 G; 1618 T; 0 other;
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                   Disclosure, Fig 4a; 96pp; English.
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Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
                                                                       29-DEC-2000; 2000US-259128P.
20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
                                                            26-DEC-2001; 2001WO-US49486
                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                                                            Jiang B,
                                                                                                                        WPI; 2002-566694/60
                        Candida albicans
                                     WO200253728-A2
                                                11-JUL-2002
                                                                                                                                                      expression
                                                                                                           Roemer T,
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Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional Ohlsen KL; Виввеу Н, Boone C,

Claim 76; SEQ ID NO 2884; 167pp + Sequence Listing; English.

The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying cons allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in which both alleles of a gene are weeful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus of the contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus of and for identifying a compound which modulates the compound catabolism, blosynthetic, transporter, transcriptional.

Compound catabolism, blosynthetic, transporter, transcriptional, translational signal transduction, DNA replacation and cell division activity. The method is useful for identifying a compound having the compound subtraction by C. albicans. The present sequence is that of a pcr reating infection by C. albicans. The present sequence is that of a pcr reating infection by C. albicans. The present sequence is that of a pcr reating in the printed and convert Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

Sequence 65 BP; 20 A; 11 C; 2 G; 32 T; 0 other;

0; Gaps 0; Indels 14.5%; Score 65; DB 24; 100.0%; Pred. No. 0.005; ive 0; Mismatches 0 1 Similarity 100. 65; Conservative Query Match Local Matches à

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AAAGA 68 AAAGA 64 S g 셤 à

RESULT 7 AAS45346/c ID AAS45346 standard; DNA; 9539

BP.

AAS45346;

(first entry) 18-DEC-2001

Chemically pretreated genomic DNA associated with cell cycle #26.

Cell cycle, human, CpG dinucleotide, cytosine methylation, HIV; aging, human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease, cancer; archritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds; PCR primer

Homo sapiens

WO200168911-A2

20-SEP-2001.

15-MAR-2001; 2001WO-EP02945.

15-MAR-2000, 2000DE-1013847. 06-APR-2000, 2000DE-10199173. 07-APR-2000, 2000DE-1019173. 30-UTM-2000, 2000DE-10338259. 01-SEP-2000, 2000DE-1043826.

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-602751/68

Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle

Claim 1; SEQ ID No 51; 28pp; English.

molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dimucleotides in a sequence and therefore for analysing sociated diseases. By analysing cycosine methylations in the pretreated both, generatic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic diagnosis and/or apigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy aging, plomerular disease, leavy body disease, graft-versus-host disease, arteriosclerosis, solid tumours and cancers. Sequences AAS45296-AAS45520 represent chemically pretreated genomic

Sequence 9539 BP; 2665 A; 121 C; 2515 G; 4238 T; 0 other;

Length 9539;

6133 4 TCAGATATAGATATAGATATGTATTAAATTTAGAAGAAGAACAATATGAATTAGGATTT ô Indels 14.0%; Score 62.6; DB 22; 47.8%; Pred. No. 0.014; ative 0; Mismatches 199; 182; Conservative Similarity Query Match Best Local Si Matches 182; 셤

6073 64 AAAGAAGGICAAATACAAGGAACAAAGATCAATATTTAGAAGGAAAAGAATATGGTTAT 6132 AAAACAAAAACGAACTTAAAAATTCAAAACACATTTTAAACTCCAAAAATAAATTATAAA

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6072 AACAAACGAAATTAAAAAATCGAAATTTAAAAATCAAAATAAAATTAAAAATTAAAATA 6013 124 CAAACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGG

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363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNA; Ortosine methylation state; SNP; retroviral infection; gene; distinction; ortosine methylation state; SNP; retroviral infection; gene; distinction; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiasis; psoriasis; Rieger's syndrome; neurological disorder; erythropoiasis; meurological disorder; erythropoiasis; myelodysplastic syndrome; myerchoburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myeorderial infarction; hypertension; arthritis; polyglutamine disorder; solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer; in particular an oligomuclectide or peptide nucleic acid (PNA) -oligomer that hybridises to or is identical transcription. The set of aligomer probes are useful for detecting the cytosine methylation state and/or single nuclectide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for
TTATCCCATATAGATCAATATAACATCTTCTTCACTTCGGAATCATTTGAATAATTTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
                                                                 GAAGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAA
                                                                                                                                       AAAAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA transcription associated genomic DNA #27
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ABK28179 standard; DNA; 9539
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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diagnosing or treating diseases associated with DNA transcription departually with the methylation status), e.g. adenosine deaminase deficiency, viral infection, status infection, Sezary syndrome, haematological disorders, immunological disorders, Werner syndrome, tuberculosis, developmental disorders, Werner syndrome, neurological disorders, neurodegenerative disorders, Maardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial infarction, hypertension, anglogenerative disorders, congenital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription solicient of the sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                   Length 9539;
                                                                                                                                                                                                                                                                 Sequence 9539 BP; 2665 A; 121 C; 2515 G; 4238 T; 0 other;
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                                                                                                                                                                                                                                                                                                 Query Match
14.0%; Score 62.6; DB 24;
Best Local Similarity 47.8%; Pred. No. 0.014;
Matches 182; Conservative 0; Mismatches 199;
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                                                                                                                                                 The present invention describes the human hypocretin (orexin) receptor 2 (HCRRE) gene (given in AAH31613), which is associated with narcolepsy. Identification of the HCRTR2 nucleic acid molecule permits the diagnosis of narcolepsy. A method from the present invention is provided for treating narcolepsy by administering to the individual an isolated HCRTR2 nucleic acid in a therapeutically effective amount so that the cells produce native HCRTR2 receptor. The diagnosis of narcolepsy has been difficult to differentiate from other conditions such as chronic facting acid makes it possible to accurately diagnose narcolepsy.
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                                                                                                                                                                                                                                                         nucleic acid makes it possible to accurately diagnose narcolepsy. AAH21541 to AAH21612 represent primers used in the identification of narcolepsy gene in an example from the present invention. AAH21613 represents the HCRTR2 gene which encodes the HCRTR2 protein given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ACTGGATTICAACGATTTTTAATCATTGGTTATTTCAAGAATTAATGAAATTTTGGTTA
                                                                              Gene for hypocretin (orexin) receptor 2 (HCRTR2) which is associated with narcolepsy, useful in methods of diagnosis of narcolepsy and
                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                             Sequence 168575 BP; 55308 A; 29672 C; 29838 G; 53757 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      Score 61.2; DB 22; Length 168575;
Pred. No. 0.025;
0; Mismatches 218; Indels 1; C
                                                                                             with narcolepsy, useful in methods of dia
pharmaceutical compositions for therapy -
                                                                                                                            Claim 1; Fig 1; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.1%;
Matches 203; Conservative (
(DECO-) DECODE GENETICS EHF
                        Gulcher J;
                                              2001-300504/31
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                                                        P-PSDB; AAB98007
                      Olafsdottir BR,
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ABL32487 standard; DNA; 17183 BP.

ABL32487;

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system discorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AnDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                 antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; neuroprotective; antiarthribit; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; atteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                               Human; immune system disease; cytosine methylation;
Human immune system associated gene SEQ ID NO: 460.
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0; Mismatches 178;
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es 185; Conservative
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Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac demage; inflammatory response; Haemophila; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; coscophageal cancer; ds; tumour; immunostimulant; cardiant; artiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                         186 ATCCCATATAGATCAATATAATAACTCTTCACTTCGGAATCATTTGAATAATTTGGA
                                                                                           246 AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA
                                                                                                                                                                                                 306 AAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTG
                                                                                                                                                                                                                                                                 366 GAAAATTGATTCATTGGATAATTTGGTGAAAGAAGTAGGTGGAACTTTACAAGTTAGTGA
                                                                                                                                                                                                                                                                                                    Human gene regulation-associated gene oligonucleotide #32.
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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3935 TATAAAAATATACCAACCCAAAAAAAAAAAATTAAAAAATAAATTATATCATTCAATA 3876
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                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; encroprotective; anti-HIV; anticonvulsant; ophthalmological; antitheumatic; antiarthritic; antidiabetic; antisportatic; antialiammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 299; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 299
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01-SEP-2000; 2000DE-1043826.
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                                                                    3875 ATCCAATÁAA 3865
                                  360 AACTIGGAAAA 370
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*tag= d transl_except= AAC encodes Aspartic acid

except= GAA encodes Glutamine

/*tag= e /transl_ex 5546..5548

misc_feature

except= CCT encodes Arginine

/transl_exc 6254..6256

misc_feature

*tag=

misc_feature

/*tag= g /transl_except= AAT encodes Lysine 6257..6259

except= ATA encodes Tyrosine

transl *tag=

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misc_feature misc_feature

product= Erythrocyte membrane protein

misc_feature misc_feature misc_feature

/*tag= b /transl except= GTA encodes Tyrosine 656..658

*tag= c transl except= ATT encodes Leucine 909..2911

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dissimilar to cytosine, to enable analysis of cytosine methylations.
The DNA sequences, oligomers (or sets/arrays) and method are useful in the disquosis of diseases for predisposition to diseases) associated with gene regulation and in therapy of such diseases, by this are provided. They are especially useful in disquosis and therapy of e.g. severe combined immunodeficiency disease, cardiac and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, werner syndrome, asthma, this syndrome, Saethre-Chorzen syndrome, renal disease, sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at.

ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1782
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*tag= m transl_except= GGA encodes Tryptophan

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intron

transl_except= ATT encodes Asparagine

except= TIC encodes Isoleucine

transl

misc_feature

misc_feature

transl except= AAC encodes Lysine 5269..6271

except= ATA encodes Histidine

/transl_ex 6275..6277

misc_feature

misc_feature

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A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte membrane protein 1 (PfEMPI) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaxia parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaxia. Nucleic acids derived from the PfEMPI gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically immunoreactive with the PEMPI polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Plasmodium falciparum erythrocyte membrane proteins - used develop products for the diagnosis, treatment or prevention of malaria parasite infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Figure 12; 149pp; English.
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P-PSDB; AAW00384.
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cDNA encoding Plasmodium falciparum erythrocyte membrane protein.

(first entry)

20-FEB-1997

AAT41852

AAT41852 standard; DNA; 9789 BP.

falciparum; erythrocyte membrane protein; malaria; identification; treatment; prevention; parasite; ss

Location/Qualifiers 326..9497

Plasmodium falciparum MC type.

Plasmodium detection;

Pasloske

Baruch DI, Howard RJ,

(AFFY-) AFFYMAX TECHNOLOGIES NV.

96WO-US05798

26-APR-1996;

27-APR-1995;

W09633736-A1

31-OCT-1996.

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WPI; 2002-130909/17
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                                                                                                                                       AGAAGGICAAATACAAGGAACAAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCA 125
                                                                                                                                                                                                                                                            246 AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGAA 305
                                                                                                                                                                                                                                                                                                   AAATATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTG 365
                                                                                                AACTGGATTTCAACGATTTTTAATCATTGGTTATTCAAGAATTAATGAAATTTTGGTT
                                                                                                                                                                                                                                                                               ATCCCATATAGATCAATATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGA
                                                                              Gaps
PfEMP1 protein of the MC type of Plasmodium falciparum. An alternative, truncated version of the coding sequence (a cDNA clone) is given in AAT41853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiansemic; cytostatic; nootropic, nentiansemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; obthtalmologic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; sy disease; arteriosclerosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                              ô
                                                         Length 9789;
                                      Sequence 9789 BP; 4061 A; 1393 C; 1837 G; 2498 T; 0 other;
                                                        Query Match 13.4%; Score 59.8; DB 17; Length Best Local Similarity 47.1%; Pred. No. 0.043; Matches 184; Conservative 0; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system associated gene SEQ ID NO: 2331.
                                                                                                                                                                                                                                                                                                                                                           8248 AAAATAAATAAAAAAAAAAAAAAAAAAAA 8278
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2000DE-1043826
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                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ANDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
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muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 PACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGTT
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acid comprising fragment of chemically modified gene, useful gnosis and treatment of diseases associated with abnormal
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                                                                                                           Claim 1; SEQ ID NO 2331; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59.8; DB 24;
Pred. No. 0.043;
0; Mismatches 227;
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Best Local Similarity 46.3%;
Matches 196; Conservative
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us-09-980-054a-11.rng

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived actation and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them.

Comprising an LMFD nucleic acid linked to a promoter and 3' non-cranisated sequence that functions in the cell to cause termination of transcription and addition of polyadanylated inbouncedides to a 3' end comprising an LMFD nucleic acid linked to a promoter and 3' non-cranscription and addition of polyadanylated inbourderides to a 3' end complement or and addition of polyadanylated inbourderides to a 3' end complement or fragment with a complementary nucleic acid (comprising any of the 1512 nucleic acid molecule for complement or fragment where hybridisation between the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid is predictive of the level or pattern of the LMFD nucleic acid is predictive of the level or pattern of the LMFD nucleic acid is bovine cell or tissue. It is useful for genome of a molecule in a bovine cell or tissue. It is useful for genome complementary nucleic acid is bread for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome complementary nucleic acid is useful present sequence is one of the 15112 bovine complement sequence tag) nucleic acids.

Complement or present sequence tage nucleic acids of the respective of the news not shown in the specification but the complementary nucleic acide the news not shown in the specification but the news obtained the news not shown in the specification but the news nucleic acide is the news obtained the news not shown in the specification but the news nucleur the news nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur nucleur n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
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                                                                                                                                                                                                                                                                                                                                                                  Tao N, Warren WC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID No 3400; 245pp; English
                                                                             24-SEP-2001; 2001US-0960352.
                                                                                                                                    12-JAN-1999; 99US-115707P.
11-JAN-2000; 2000US-0480902.
                                                                                                                                                                                                                                                                                                                                                            Byatt JC, Mathialagan N,
                                                                                                                                                                                                                  (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                        (TAON/) TAO N.
(WARR/) WARREN W C.
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                               26-SEP-2002.
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66 AGAAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCA 125
                                                                                                                                                                 126 AACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTGGTT 185
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Query Match 13.3%; Score 59.4; DB 25; Length 446; Best Local Similarity 47.7%; Pred. No. 0.05; Matches 174; Conservative 0; Mismatches 191; Indels 0.
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246 AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA 305
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Search completed: February 16, 2004, 11:20:19 Job time : 281 secs AL565455

BX415878 BX415878
AL069706 Drosophil
BX462207 BX462207
BH180166 016 I 02BX433779 BX433779
BX335216
AL106396 Drosophil
CD0496847 Drosophil
CD049684 AGENCOURT
AL106893 Drosophil
AL109318 Drosophil
AL109318 Drosophil
AL23458 Tetracdon
BX4638 BX415318
CC218891 CH26.-14M
BX415231 BX415231
AQ89737 H3 3153
AL532464 AL53346
BJ33457 BJ33457
BJ33457 BJ33457
BJ33457 BJ33457
BJ33457 BJ33466
BX355654 BX355654
AL234027 Tetracdon
AL241028

BX335216 CNS0167M CNS00EA9 CD049644 CNS0155H CNS0155H CNS038CX AL54336 CNS038CX BX446388 CC218891 BX415231 AQ897537

AL532464 BJ333457 AG136199 BJ335466 BJ394994

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Candida tropicalis

Candida tropicalis

Candida tropicalis

Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 1059)

Is Souciet, Ji., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Pukuhara, M., Bon, E., Brottier, P., Casaregolas, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

AL FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1059 bp DNA linear T3 end of clone XBD0AA002E07 of library XBD0AA from of Candida tropicalis, genomic survey sequence. A441526.1 GI:12224752
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DEFINITION
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AL417187 T3 end of
BX414650 BX414650
AL060732 Drosophil
                                                          February 16, 2004, 10:54:01; Search time 2562 Seconds (without alignments) 4240.477 Million cell updates/sec
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                       22781392 seqs, 12152238056 residues
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                     OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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CNS06VIL
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CNS001FB
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HI80441 016 H 20-AL61739 T3 end of AL61739 T3 end of AL017865 Drosophil BX331505 AL402900 T3 end of BX421282 BX421282 AL217579 Tetraodon BH130447 ENTOPISTF AL061936 Drosophil BX387370 BX387370 BX387370 AL532464 AL522464 AL522464 AL522464 AL522464 AL522464 AL522464 AL522464 AL522464

BH180441 CNS007MAN CNS00DKY BX331505 CNS06KHQ BX421282 CNS020WVM BH120002147 CNS002147

GSS 08-JUL-2001 strain CBS 94

ALIGNMENTS

2 (bases 1 to 1059)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
Dujon,B.

11152876

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Local Similarity
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                                                                                                                                                          This diston Cremieux, 05706, 91057 BVRY cedex, PRANCE. (B-mail: sequencedee, cons.fr - Web: 1057 BVRY cedex, PRANCE. (B-mail: sequenceope.cns.fr - Web: 1057 BVRY cedex, PRANCE. (B-mail: sequenceope.cns.fr - Web: 1057 BVRY cedex, PRANCE. (B-mail: This dSS is part of a random genomic sequencing program of thirteen yeast species: Saccharcomyces bayanus var. uvarum, Saccharcomyces servazzii, Zygosaccharcomyces rouxii, Saccharcomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia anguera, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to keywords for describtion of this sequence and for the sequence of the other extremity of this insert.
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                                                                                                        Genoscope.

Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

^ --- Aston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (B-mail
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<26. .>346)
/note="8imilar to Saccharomyces cerevisiae ORF YNL260c
hypothetical protein ]"
Genomic exploration of the hemiascomycetous yeasts: 16. Candida
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Pred. No. 1.3e-16;
1; Mismatches 99; Indels
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mol_type="genomic DNA"
strain="CBS 94"
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                     tropicalis
FEBS Lett. 487 (1), 91-94 (2000)
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clone="XBD0AA002E07"
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note="end : T3"
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tal Similarity 72.8%;
267; Conservative
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                                                                                                          AUTHORS
TITLE
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Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
8 egrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces bayanus var. uvarum, Saccharomyces
lactis var. lactis, Kluyveromyces thermocolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
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end of clone AXCAA021C12 of library AXCAA from strain CBS 7064 Pichia farinosa, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                    Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Caearegola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Caearegola, S.,
de-Montigary, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuvelise, C., Ozie--Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Montigmy, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B., Wincker, P., Artiguenave, F. and Potier, S. Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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Pred. No. 2.4e-05;
1; Mismatches 125; Indels
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FEBS Lett. 487 (1), 87-90 (2000)
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/strain="CBS 7064"
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/clone="AX0AA021C12"
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/note="end : T3"
                                                                                                AL417187.1 GI:12198580 GSS.
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al Similarity 60.8%;
209; Conservative 1
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                                                                                                                                                                                  Pichia farinosa
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Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 ENYY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovo Googgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RepCT-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST library is named RepCT-98 and was constructed by partial and how to order individual BAC clones, the entire library or found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                             GSS 03-JUN-1999
                                                                                   TATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGGAA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR04A23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 AAAGAAGGTCAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTAT
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
EbyVaroidea; Drosophilidae; Drosophila.
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Pred. No. 0.79;
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                                                                                                                                                                       369 AATTGATTCATTGGATAATTTGGTGAAAGAAGTA 402
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/clone lib="kPCT-98"
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87414650 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAPOO1YNO2
3-PRIME, mRNA sequence.
BX414650
TIAICCCAIAIAGAICAAIAIAAIAACICTICTICACTICGGAAICAITIGAAIAAITIG 243
                                                   734 TIGICICAGIATGAGCAAAIAGTIAGCAITAAGACACIAGAAAAICACTIAAGICIGGCA 793
                                                                                                                       GAAGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAA 303
                                                                                                                                                                              GAAGGCATTTTGGATGGCATTTCTATGGAWAATACGGAAGATGCTGTAAGAGAGTATGAA 853
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 910 GENZY cedex - France
Email: Seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6015.f
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://tullength.livitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001DG01NP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Pred. No. 0.39;
3; Mismatches 108;
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121 c 25 g 324 t
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Mammalia; Eutheria; Primates;
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Best Local Similarity 23.10,
-Loc 77; Conservative 149;
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BX415878 1100 bp mRNA linear EST 15-MAY-2003 4X15878 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008Y104 5-PRIME, mRNA sequence.
BX415878
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/clone_lib="Homo sapiens THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT_6" ist strand cDNA was primed with a NotI-oligo(d7) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized." 170 others
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1 (bases 1 to 1200)
1 'Ly Ba, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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                                                                                                              TGGTTATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAAT
                                                                                                                                                241 TTGGAAGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTAT
                                                                                                                                                                                                                                                                                                 301 GAAAAAATTITAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAA
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Linvitrogen. Contact : Feng Liang Email : fliang@lifetech.com U
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP008BE02CPP1.
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41.2%; Pred. No. 1.6;
ive 44; Mismatches 180;
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/db_xref="taxon:9606"
/clone="CSOCAP008Y104"
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Best Local Si
Matches 157,
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BX415878/c
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1201 bp mRNA linear EST 12-MAY-2003
AL565455 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODF005YO18 3-PRIME, mRNA sequence.
AL565455
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=GSODF005BH09NPL&cluster=9232.f. Contact:
Feng Liang Email: fliang@lifecech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF005BH09NPl.
LocationfQualifiers
744
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/dev stage="fetal"
/dov stage="fetal"
/clone_lib="Home sapiens FETAL BRAIN"
/note="lorgan: brain; Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

82 c 71 g 313 t 185 others
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
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                                                                                                                                                                                                                                                             364 TGGAAAATTGATTCATTGGATAATTTGGTGAAAGAAGTAGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'organism="Homo sapiens"
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db_xref="taxon:9606"
clone="CSODF005Y018"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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Best Local Similarity 36.6%; Pred. No. 2.3;
Matches 159; Conservative 76; Mismatches 197; Indels
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ALO69706
ALO69706.1 GI:4949849
          AGGICAAATACAAGGAACAAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCAAAC 128
                                 129 TGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTTGGTTATC 188
                                                                    189 CCATATAGATCAATAAAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAGA 248
                                                                                                                           249 TATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAAAA 308
                                                                                                                                                                  309 TATTAAAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGGAA 368
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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db xref="taxon:7227"
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16.6%; Score 74.4; DB 29; Length 1101;

Query Match

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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 24.r. For more
information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODG004CA02QP1&cluster=24.r. Contact :
Feng Liang Email : fliangeliferech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG004CA02QP1.
Location/Qualifiers
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BX462207 GI:31023422
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                                                                                                  367 AAAATTGATTCATTGGATAATTTGGTGAAAGAAGTAGGTGGAACTTTACAAGTTAGTGAA 426
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
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/cell line="RAMOS CELL LINE"
/clone lib="the"Homes CELL LINE)"
/note="Type-tor: pCMVSPORT_6, 1st strand cDNA was primed
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/db_xref="taxon:9606"
/clone="CSODG004YB03"
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/strain="Puerto-Rican"

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Matches 184;
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with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

177 others
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Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
Genomics 65 (2), 87-94 (2000)
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Strigeidida, Schistosomatoidea, Schistosomatidae, Schistosoma.
1 (bases 1 to 725)
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                                                                                                     Length 1201;
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1 rue du Professeur A. Calmette, 59019-Lille, France

1 (3) (0)3 2087788

Fax: (33) (0)3 20877888

Email: Raymond.Pierce@pasteur-lille.fr
                                                                                                                                Indels
                                                                                              Query Match
16.6%; Score 74; DB 13; Le
Best Local Similarity 44.9%; Pred. No. 2.5;
Matches 149; Conservative 29; Mismatches 154;
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/mol_type="genomic DNA"
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Plate: 016 row: I column: 02
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genomic survey sequence.
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High quality sequence stop: 725.
Location/Qualifiers
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Seg primer: M13 -21 primer
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Contact: Pierce RJ
INSERM U 167
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BH180166.1 GI:16281799
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Schistosoma mansoni
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/dev stage="cercariae"
/dev stage="cercariae"
/dab_host="Biomphalaria glabrata"
/lab_host="Biomphalaria glabrata"
/clone lib="BombAcI 11; Site 1: Hind III; Partially
Inote="Wector: pBeloBAC 11; Site 1: Hind III; Partially
Hind III digested and size=selected 8. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 2380s clones from 4 independent
sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."
51 a 52 c 39 g 420 t 63 others
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 AAAAGGCAAGAAATAAATTAAGAGTGATAGCTAGTATAACTAAAGAAACTTGGAAAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ATATAGATAATGTATTAAATTTAGAAGAACAATATGAATTAGGATTTAAAGAAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 TAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGAAGATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 TWWTTRGAAAWAAWTATTATTAAGTATAATRATRTATWTAAAATTAAATAAAAWATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 AITCAITGGALAATTIGGIGAAAGAAGIAGGIGGAACITIACAAGITAGTGAAAACCCCG
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                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 72.4; DB 28; ilarity 42.8%; Pred. No. 4.6; Conservative 30; Mismatches 216;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
/db_xref="taxon:6183"
/clone="016102"
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Homo sapiens
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Best Local Similarity
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FEATURES
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                                                                                                                                                                                                                                     /mol_type="wRNA"
//db xxef="texon:966"
/clone="CSODEDAYFO5"
/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSFORT 6; 1st strand cDNA was primed
/note="Vector: pCMVSFORT 6; 1st strand cDNA was primed
with a NotI-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
150 c 207 others
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BX335216 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI012YG10 5-PRIME, mRNA sequence.
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Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3370.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi/seq=CSODE014CCO3NP1&cluster=3370.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE014CCO3NP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Mismatches 196; Indels
                                                                                                                                                                                                                  organism="Homo sapiens"
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BX335216/c
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CNSO167M linear GSS 26-UUL-1999 DNA linear GSS 26-UUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN15M24 of DrosbAC library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="teaxon:9606"
/clone="CSDD1012YG10"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone="Lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone="list strand oDNA was primed with a NorI-oligo(dT)
/note="list strand oDNA was primed with a NorI-oligo(dT)
/note="list strand oDNA was primed with a NorI and EcoR odigested with Nor I and cloned into the Not I and EcoR odigested with Nor I and cloned into the Nor I and EcoR odigested with Nor I and ScoR odies of the NorWebRT 6 vector. Library was normalized."

a 115 c 137 g 453 t 105 others
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                                                                                                                                                                                                                                                                                                                                                         http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSODIOI2BD05QP1&cluster=714.f. Contact
Feng Liang Bmail : flang@lifetech.com URL i
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI012BD05QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AGAAGGICAAATACAAGGAACAAAGATCAATATTTAGAAGGAAAAGAATATGGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AACTGGATTTCAACGATTTTTAATCATTGGTTATATTCAAGAATTAATGAAATTTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 ATCCCATATAGATCAATATAATAACTCTTCTTCACTTCGGAATCATTTGAATAATTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%; Score 71.2; DB 13; Length 1201;
llarity 43.6%; Pred. No. 5.4;
Conservative 33; Mismatches 188; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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AL106396
AL106396.1 GI:5621701
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                                   (bases 1 to 1201)
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JOURNAL
COMMENT
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Droject grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drangaster genome survey sequence TET3 end of BAC # BACR28K21 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                             Drosophila melanogaster

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota, Neoptera, Euchopera, Diptera, Brachycera; Muscomorpha; Ephydroidea, Drosophila.

1 (bases 1 to 1201)
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                   Orosophila melanogaster (fruit flv)
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/plasmid="pBeloBAC11"
/note="end : T7"
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"Web: www.genoscope.cns.trn."

- Web: www.genoscope.cns.trn.

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osocgaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RECI-98 and was constructed by partial BCORI digetion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be located that the part of the library is comed at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
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db xref="taxon:7227"
/clone="back28K21"
/clone lib="RPOT-98"
/note="end : TET3"
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1 (bases 1 to 997)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="NIH MGC 172"
/note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
LIBR PRIMING - oligo dT; METHOD - full-length enriched;
Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"
128 c 113 g 306 t 23 others
                                                                                                                                                                                                                                   Email: capbs=r@mail.nib.gov
Tissue Procurement: Dr. Jamie Thompson, University of WI
Fissue Procurement: Dr. Jamie Thompson, University of WI
CDNA Library Preparation: Ghaz Zastrow-Hayes
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDKM47 row: e column: 22
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High quality sequence stort: 10
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/lab_host="DH10B TonA"
mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Homo sapiens"
                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
 397 bp
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'db xref="taxon:9606"
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46.8%;
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LUVI DP DNA linear GSS 26-JUL-1999 Brosophila melanogaster genome survey sequence SP6 end of BAC BACN13C23 of DrosBAC library from Drosophila melanogaster (fruit ALI), genomic survey sequence.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bullend at CEPH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (3-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 AGATATTATGGCACAAATTTCTATAACGAATGGAGATAAAGAAGTTGAAGATTATGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
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/ Organism="Drosophila melanogaster"

/mol type="genomic DNA"

/db_xref="taxon:7227"

/clone="pack"

/plasmid="pbelobAc11"
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Job time : 2569 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 16, 2004, 14:27:58 ; Search time 2528 Seconds (without alignments) 1422.889 Million cell updates/sec
OM protein - nucleic search, using frame_plus_p2n model
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772
1 MSDIDIDNVLNLEEEQYELG.......NLVKEVGGTLQVSENPDDMW 148 22781392 segs, 12152238056 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Minimum DB seq length: 0 Maximum DB seq length: 2000000000 **BLOSUM62** Title: Perfect score: Scoring table: Sequence: Searched:

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		41526 T3 end o	.7187 T3 end o	36387 CG2026.E	10548 KD0783.R	1456 17 em	2715 OSIIED11	1520 HD04B05r	58430 HB07H22	72468 HB09H22	1649 70149912	92706 PUEBB09	CA764105 AF53-Rp	13233 AV913233	271	405283 PUHTB6/T	320/5 AU432U	1938 HVSME	PROCEAUSYS BINI 9 CO	SEAS INTERIO	2576 LERGG	15171 3529	.5339 EST60	7388 146664	5637 EST46	9966 EST504	5065 EST57	5338 EST600	2791 EST53	3616931 602615	792 EST175	46 ZCZ /DUB.	146//1 7104103 7654530 27874	2319 III -R-F	5233 RC5-CI	BU662888 c192q0	1310 K-ESTC	4554 DKFZp6	9788 K-EST013	9687 EST37175	155 AV682155	7075 K-ESTO	B50088 K-EST013	
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ALIGNMENTS

CNSO7EAO 11059 bp DNA linear GSS 08-JUL-2001 T3 end of clone XBD0AA002E07 of library XBD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence. AL441526.1 GI:12224752 GSS. AL441526 RESULT 1 CNS07EAO/c LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS

Candida tropicalis Candida tropicalis Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida. 1 (bases 1 to 1059)

REFERENCE

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61 TrpLeuSerHisIleAspGlnTyrAsnAsnSerSerLeuArgAsnHisLeuAsnAsn 80
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazii, Sygosaccharomyces roundii,
Saccharomyces servazii, Sygosaccharomyces roundii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See kb were prepared and both extremities were sequenced.
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Blandin, G., Ozier-Kalogeropoulos, O., Wincker, P., Artiguenave, F. and
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrans, P., Lepingle, A., Libcente, B., Malpertuy, A., Neuvelise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                              Genomic exploration of the hemiascomycetous yeasts: 16. Candida tropicalis
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Matches:
Conservative:
Mismatches:
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/note="end : T3"
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Libratical (107-SEP-2000) Genoscope - Centre National de Sequencage, Submitted (107-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequescagenoscope.cns.fr. www.genoscope.cns.fr]
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvartum, Saccharomyces ervazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii, var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSOGVIL 902 bp DNA linear GSS 06-JUL-2001 T3 end of clone AXOAA021C12 of library AXOAA from strain CBS 7064 of Pichia farinosa, genomic survey sequence.
                                                                                      81 LeuGluAspileMetAlaGlnileSerileThrAsnGlyAspLysGluValGluAspTyr 100
187 TGGTTGGATAATCTAGACAACTATAATGCTTCCAAATCACTTCAAGGTCATATAAATCAA 128
                                                                                                                                                                                                                                                                                              101 GluLysAsnijeLysLysAlaArgAsnLysLeuArgValileAlaSerileThrLysGlu 120
                                                                                                                                                                                             127 CTAAGTGAACTAATAACTGACATACCATTGACAAATGGAGATGAAGAAGTTGAAAAATAC 68
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Souciet, J.L., Aigle, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
FEBS Lett. 487 (1), 3-12 (2000)
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Saccharomycetales, Saccharomycetaceae, Pichia.
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de Montigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Potier, S.
Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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/mol_type="genomic DNA"
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GSS 31-OCT-2002
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Kluyveromyces delphensis
Kluyveromyces delphensis
Kluyveromyces delphensis
Bukaryota; Rungi, Ascomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetacees; Kluyveromyces.

1 (bases 1 to 433)
Wong, S., Fares M.A., Zimmermann, W., Butler, G. and Wolfe, K.H.
Evidence from comparative genomics for a complete sexual cycle in the 'asexual' pathogenic yeast Candida glabrata
Genome Biol. 4 (2), R10 (2003)
                                                                                                                                                                                                                                                               24 GlyGlnIleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThr 43
                                                                                                                                                                                                                                                                                                                               44 GlyPheGlnArgPheLeullelleGlyTyrIleGlnGluLeuMetLysPheTrpLeuSer 63
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KD0783.R1 Kluyveromyces delphensis Random Genomic Library
Kluyveromyces delphensis genomic clone KD0783, genomic survey
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Department of Genetics, Smurfit Institute
Trinity College Dublin
Dublin 2, Ireland
Tel: 353 1 6082319
Rax: 353 1 679858
Email: swongercd.ie
Class: plasmid ends.
Location/Qualifiers
                                                                  Matches:
Conservative:
Mismatches:
Indels:
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57.64%
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25.97%
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180 GGAGAAATCAAA 169
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|34 TIGICICAGIATGAGGAAATAGTTAAGACACTAAGAAAATGACTTAAGTCTGGCA 793
                                                                                                                                                                                                                               614 CAAGGAGTCTTTGTTCAGGAGCTGCATTTGGAAGGAATGGAATATGGTTATCAAACAGGC 673
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/clone="CG2026"
/clone_lib="Candida glabrata Random Genomic Library"
127 c 85 g 214 t
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Contact: Wong s
Department of Genetics, Smurfit Institute
Trinity College Dublin
Dublin 2, Ireland
Tel: 353 1 6082319
Tel: 353 1 6798558
Email: swong@tcd.ie
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mol type="genomic DNA"
fetrain="CBS 138"
   296 t
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                                                           8.28e-26
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Balcaromycetales; Saccharomycetaceae; Pichia.

Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Gelmontigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycerous yeasts: 1. A set of yeast species for molecular evolution studies

L FEBS Lett. 487 (1), 3-12 (2000)

11152876
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                                                                                                                                                                                                                                                                                                                                                           49 ATGGATGTTGATGTTATTTTTAGAGGAGAGTTTTACAAGAAGGCTACCAAGAA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GGTAGAAGTGAAATTTAAAGAACAATCTCCTTGAAGGTAAGGAATTTGGTTTACAAGTA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 AspileMetalaGinileSerileThrAsnGlyAspLysGluValGluAspTyrGluLys 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 GAACTAATCAGCACAATACAATTCAATAACGAAGAAAATGTGGAAAAGGCCTTGAAAAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 AAATTGGTTAAACTTAAAATAAGTATAGGTTAATATTGCTAGCTTTTCAAAGGGAATAT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 AsnilelysiysAlaArgAsniysLeuArgValileAlaSerIleThriysGluThrTrp 122
                                                                                                                                                                                                                                                                                                                                    4 IleAspIleAspAsnValLeuAsnLeuGluGluGluGluGlnTyrGluLeuGlyPheLysGlu 23
                                                                                                                                                                                                                                                                                                                                                                                                    24 GlyGlnIleGlnGlyThriysAspGlnTyrLeuGluGlyLyFyFGluTyrGlyThr 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 GlyPheGlnArgPheLeullelleGlyTyrlleGlnGlubeuMetLysPheTrpLeuSer 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 HislleAspGlnTyrAsn---AsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGlu 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic
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/clone_lib="Kluyveromyces delphensis Random.
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6126
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Pichia angusta
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Genoscope.

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                  exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia sungusta, Debaryomyces hansenii var. hansenii, Pichia subitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
(bases 1 to 1030)
ndin,G., Llorente,B., Malpertuy,A., Wincker,P., Artiguenave,F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(<43. .>222)
/note="similar to Saccharomyces cerevisiae ORF YNL260c
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Saccharomyces exiguus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                              Genomic exploration of the hemiascomycetous yeasts: 13. Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AspileAspIleAspAsnValLeuAsnLeuGluGluGluGluTyrGluLeuGlyPheLys
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/evidence=not_experimental
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                                                                                                                               FEBS Lett. 487 (1), 76-81 (2000)
20584723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
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CB612715 784 bp mRNA linear EST 08-APR-2003 OSIIEb11C06.r OSIIEb Oryza sativa (indica cultivar-group) cDNA clone OSIIEb11C06 3', mRNA sequence.
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Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, B.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 4 hrs after innoculation with Rice Blast (PO6-6-3)" 186 c 136 g 234 t
                                                                                    202 CGTTCTTTGATTAACGAGGTTGGCATGAAATGATGAAAATGTAGAAATTAGWW 261
                                                                                                                                                    102 LysAsnileLysLysAlaArgAsnLysLeuArgValileAlaSerileThrLysGluThr 121
                                                                                                                                                                                               262 AAGATAATGATTAAWCTGAAAAACAAATTTAGAACTATTATGATAACATTCCAAAGAATT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae, Oryza.
          148 CTAGATTCCTTAGATCTGWWGAGTAAT-----GCATTAAGTAAAAATGTTCAAAGTGTA 201
                                                        82 GluAspIleMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGlu 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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                                                                                                                                                                                                                                                                                              322 ATGAAGAAGGATAAAAGAGAACCATTTACCTTTGAAGTT 360
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row. C column: 06
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
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Tel: 520 626 3967
Fax: 520 621 9288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct outmitted (07-SEP-2000) Genoscope - Centre National de Sequencage, Direct Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefégenoscope.cns.fr) - Web. genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces cataromyces rouxii, Saccharomyces servazzii, Zygoaccharomyces rouxii, Saccharomyces servazzii, Zygoaccharomyces rouxii, Saccharomyces kluyvering servazzii, Pichias sacharomyces hansenii ansenii Pichia sangusta, Debaryomyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the other extremity of this sequence and for the sequence of the other extremity of this insert.
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 849)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Wontigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Sautin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
PEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 LysGluGlyGlnIleGlnGlyThrLysAspGlnTyrLeuGluGlyLysGluTyrGlyTyr 41
                                                                                                                                                                                                                                                                                                                2 (bases 1 to 849)
Bon,E., Netweglise,C., Lepingle,A., Wincker,P., Artiguenave,F.,
Galilardin,C. and Casaregola,S.
Genomic exploration of the hemiascomycetous yeasts: 6.
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/strain="CBS 379"
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108 c 159 g 253
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/dev_stage="callus (5-10 mm in diameter)"
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/clone_lib="xx110-Gold"
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Hordeum vulgare
Hordeum vulgare
Hordeum vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Permatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
1 (bases 1 to 606)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ461520 606 bp mRNA linear EST 30-MAY-2002
HD04B05r HD Hordeum vulgare cDNA clone HD04B05 5-PRIME, mRNA
                                                                                                                                     533 GGAAAAGAAGAGAAAGCTAGGTTTAAAGAATGGTTTTCAGGTAAGAGAATA 474
||||:::|||
TTAGATGAGACACACTATGAAAGGGTTTCAAGAATGGTTATAGTGAGGGCTTGGTGTCT 534
                                                                                                                                                                                                                                                                      473 GGTTTTTATCAGGGATGTCTGGATGTTTGGACGTCGTTGGTTTCAATTGATCAAGATGCA 414
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353 ITGTCGAACCCAGAAGGAAGTTCAAGATATA-----ATGGAGAAGATAAGA 303
                                                                                                                                                                                                               GlyTyrIleGlnGluLeuMetLysPheTrpLeuSer-----HisileAspGlnTyrAsn 69
                                                                                                                                                                                                                                                                                                                                       70 AsnSerSerSerLeuArgAsnHisLeuAsnAsnLeuGluAspIleMetAlaGlnIleSer 89
                                                                                          GlnTyrLeuGluGlyLysGluTyrGlyTyrGlnThrGlyPheGlnArgPheLeullelle 51
                                                                                                                                                                                                                                                                                                                                                                              90 ileThrAsn---GlyAspLysGluValGluAspTyrGluLysAsnIleLysLysAlaArg
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AsniysLeuArgVallleAlaSer-IleThrLysGluThrTrpLysile 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 CTGAAATTCAGGGTTATCACAGCAAGTTTAGGTACAAAACTGGAGTATC 254
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Insert Length: 606 Std Error: 0.00
Plate: 4 row: B column: 5
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cultivar="Golden Promise"
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clone="HD04B05"
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BASE COUNT ORIGIN

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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU968430 611 bp mRNA linear EST 22-OCT-2002 HB07H22r BC Hordeum vulgare subsp. vulgare cDNA clone HB07H22 5-PR1MB, mRNA sequence. BU968430 GI:24219223 EBU968430.1 GI:24219223
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Radchukses 1 to 611)
Barley ESTs from developing seeds
Unpublished
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnster. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
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  db_xref="taxon:112509"
/clone="HB07H22"
fissue_type="developing caryopsis"
fvs stage="8-15 DAP (days after pollination)"
lab_host="XL10-Gold"

    611
    70xganism="Hordeum vulgare subsp. vulgare"
/mol type="meNA"
/cullivar="barke"

Matches:
Conservative:
Mismatches:
Indels:
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Insert Length: 61 Std Error:
Plate: 7 row: H column: 22
Seq primer: Ml3rev.
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                   122.00
51.35%
28.83%
15.80%
                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Location/Qualifiers

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Query Match:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pocideae;
Triticeae; Hordeum.
1 (bases 1 to 641)
Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Barley ESTs from developing seeds
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); developing caryopsis (B-15 DAP(days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinates is not 100% reliable."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 CTTGAACCAATGGTAGCCTTAGACGAGACACATTATCAAGATGGTTACAAAGATGGTTAT 319
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500 CTICTAAGCAACTATCCTITGTCT----GATCCAGAGAATAATCAGCTTCAAGACATG 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 IleMetAlaGlnIleSerIleThrAsnGlyAspLysGluValGluAspTyrGluLysAsn 103
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5-PRIME, mRNA sequence.
BQ472468
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnserr. 3, 06466, Gatersleben, Germany
Tel: 039482-5552
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Insert Length: 641 Std Error: 0.00
Plate: 9 row: H column: 22
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/clone lib="BC"
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701499129 A. thaliana, Ohio State clone set Arabidopsis thaliana
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Arabidopsis thaliana
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Dolicky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D. Arabidopsis thaliana Gene Expression MicroArray
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BZ992706.1 GI:29235764
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                                                                                  Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Genome Systems, Inc., a wholly owned subsidiary of Incyte Harmacouticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
Location/Qualifiers
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Mismatches:
Indels:
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CA764105

AF53-Rpf 02 E02 T7 003.abl IRRI Drought Stress Panicle Library Oryza sativa (indica cultivar-group) cDNA clone C0000482 5' similar CA764105. GI:27545938
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Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnic,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.
Maize Genomics Consortium
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                                                                                                                                                                                                                                                                       International Rice Information System (IRIS; http://www.iris.irri.orgj: DQ200481 Assignment of putarive function to the sequence by S. Rudd of the Munich Information Center for Protein Sequences (http://mips.gsf.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GGTTTAAAGAATGGTTTTCAGGTAGGTGAAGAACTAGGTTTTTATCAGGATGTCTGGAT 109
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                                                                                               On Dec. 2, 2002 this sequence version replaced gi:25993360. Contact: Richard Bruskiewich
Biometrics and Bioinformatics Unit
International Rice Research Institute
DAPO 7777, Merco Manila, Philippines
Tel: +63.2-845-0563
Pax: +63-2-845-0606
                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Oryza sativa (indica cultivar-group)"
                    Bennett,J., Arumugam,K., Lafitte,R., Wen,J., Rudd,S. and
Bruskiewich,R.M.
IRRI Drought Stress Panicle cDNA Library
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                         EST 18-JAN-2002
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566 bp mRNA linear EST 18-JA 4V912233 K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots Hordeum vulgare subsp. vulgare cDNA clone bagas21f7 5', mRNA sequence.
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Barley EST sequencing project in NIG and Okayama Univ
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Fax: 81-559-81-6856
Email: tahinisegenes nig.ac.jp.
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Center For Genetic Resource Information
National Institute of Genetics
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
1 (baese 1 to 648)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
perween rice and Magnaporthe grisea
648 bp mRNA linear EST 08-APR-2003 OSIEBb11C06.f OSIEB Oryza sativa (indica cultivar-group) cDNA CIONE OSIEBb11C06 5', mRNA sequence.
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378 TTAGATGAGACACACTATCAAACGGGTTTCAAGAATGGTTATAGTGAGGGCTTGGTGTCT 437
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Arizona Genomics Institute
Arizona Genomics Institute
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Exx: 520 621 9288
Email: http://genome.arizona.edu
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Conservative:
Mismatches:
Indels:
Gaps:
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: C column: 06
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. 1	USIVQI PRELIMINARY; PRT; 134 AA. OSY701:	(TrEMBLrel.	(TrEMBLrel. 12,	_	1 15.5 kDa protein.	SPCC191.08.	Schizosaccharomyces pombe (Fission yeast).	Eukaryota; Fungi; Ascomycota: Schionarymanos.	Schizosaccharomycetales: Schizosaccharomycetes;	Schizosaccharomyces.	NCBI TaxID=4896;		SEQUENCE FROM N.A.	STRAIN=972h-;	Lyne M., Rajandream M.A., Barrell B.G. Volckaert G.		EMBL; AL049644; CAB41054.1;	GeneDB_SPombe; SPCC191.08;	ical protein.	SEQUENCE 134 AA; 15485 MW; D3CE4F6135531AF0 CRC64;	Ouery Match 17.1%; Score 132; DB 3; Length 134; Best Local Similarity 28.0%; Pred. No. 0.0041; Matches 37; Conservative 29; Mismatches 58; Indels 8; Gaps 5;	LMKFWLS 63		64 HID-QYNNSSSLRNHLANLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASIT 118	61 EENSQHPKIKKAHRHLEQLKSLLESLP-TNNELEETDAGFDSYWNKITAKAKVVSSLLGT 119	119 KETWKIDSLD 128	: 120 KILPAEKIDAND 131
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71 SSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVIASITKETWKIDSLDNL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 NLEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 NMQRRVKE-GYRDGIDAGKAVTLQQGFNQGYKKGAEVILNYGRLRGTLSALLSWCHLHNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; EC022043; AAH22043.1; -
Hypothetical protein.
SEQUENCE 226 AA; 25313 MW; 8A40E87864E3F14C CRC64;
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Li Y., Wu T., Xu S., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human liver cancer tissue.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ARZZGO46; AARGS946.1;
SEQUENCE 226 AA; 25299 MW; 4031333215381E79 CRC64;
                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 10-OCT-2002 (TrEMBLrel. 22, 14) Prothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TERMBLEEL 15, 01-OCT-2000 (TERMBLEEL 15, GK003.
117 ITKETWKIDSLDN 129
                                                            122 LTSVQLGLQTKEN 134
                                                                                                                                                                                                                     PRELIMINARY;
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TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LEEEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLS--HIDQYN 69
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Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Gloeckner G., Eichinger L., Parra G., April J.F., Gilgo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and Analysis of Chromosome 2 of Dictyostelium.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ACI16032; AAL93047.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 DIDNVLNLEBBOYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSH
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Eksaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enchartoideae; Oryzeae; Oryza.
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STRAIN=cv. Nipponbare;
STRAIN=cv. Nipponbare(T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC clone:P0681F05.";
SUBMICTEG AJAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004674; BAC45146.1; --
SEQUENCE 144 AA; 16311 MW; DF840964D704F90B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
16.7%; Score 129; DB 10; Length 144;
Best Local Similarity 31.5%; Pred. No. 0.0076;
Matches 34; Conservative 23; Mismatches 45; Indels (
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139 AA; 16031 MW; A2BD240D720FDFA1 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Hypothetical 16.0 kbg protein.
Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
                                                                                                                                                                          Last sequence update)
Last annotation update)
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5 protein,
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Best Local Similarity 24.8<sup>1</sup>
Matches 33, Conservative
                                                                                PRELIMINARY;
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SEQUENCE 13
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P0681F05.15.
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01-MAR-2003
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QBT1X1;
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             RESULT 2
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37 KEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNNSSSLRNHLNNLEDIMAQISITNGDKE 96
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                                                                                                                                                                                                                                                                  Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R., Palmer N., Haft D., Rosa P., Stevenson B., Stevenson B., Abacterial genome in flux: The twelve linear and nine circular extrachromosomal DMMs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi.";

Mol. Microbiol. 0.0 (1999)

EMBL: AE001578; AAF07545.1;

InterPro: IPR003900; KID. repeat.

Pfam; PR003204; KID. speat.

Hypothetical protein; Plasmid.
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MMOI. Microbiol. 0:0-0(199)

MMEL, AE001581, AAF07675.1;

InterPro; IPR003900; KID_repeat.

Pfam, PF02524; KID, FP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                  Plasmid cp32-6.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxD=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid cp32-9.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 VEDYEKNIKKARNKIRV-IASITKE-TWKIDSLDNLVKEVGGTLQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 IDNVEKOLNEKIDGLNIKIDNVEKSELNAKIDSEDTKIDNVEKOLNI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.8%; Score 99; DB 2; Length 222; 30.2%; Pred. No. 2.8; cive 22; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.4%; Score 96; DB 2; Length 179; 31.2%; Pred. No. 3.8;
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222 AA; 25444 MW; IE7F5A0EAA303BDE CRC64;
                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                    -MAY-2000 (TrEMBLrel. 13, Created)
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                                     PRELIMINARY;
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Best Local Similarity
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RESULT 6
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Best Local Similarity

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                                                                                                     7 RIYDIBSIKNEFLNIGFSEBAIDFVFLHNDNY-NYEVLKEKIIDVEKNL-QKDISSLDTK 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M., Aksoy S.,
8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.4%; Score 96; DB 16; Length 223;
Best Local Similarity 27.6%; Pred. No. 4.9;
Matches 40; Conservative 27; Mismatches 46; Indels 32; Gaps
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MEDLINE=201960GP, PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Wigglesworthia.
NCBI_TaxID=164609;
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                                                                                                                                                                                                    97 VEDYEKN----IKKARNKLRV-IASITKE-TWKIDSLDNLVKEVGGTLQ 139
                                                                                                                                                                                                                                            65 IDDNVEKNLNVKIDNVEKNLNIKIDSVKNELNSKIDSLDTKIDNVEKTLQ 113
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CG13175 OR CG13174.
Drosophila melanogastra (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Bukaryota, Endopteray, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
20; Mismatches 47; Indels
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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34; Conservative
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George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen I.X., Randon R.C., Ragers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G., Andrews-Feanmankoch C., Baldwin D., Ballew R.M., Basu A. An H.-J., Andrews-Feanmach, C., Baldwin D., Ballew R.M., Basu A., An H.-J., Andrews-Feanmach, C., Baldwin D., Ballew R.M., Basu A., Baxandlae J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Bauler H., Cadieu E., Center A., Charita I., Andrews D., Bauller H., Cadieu E., Center A., Chara I., Burtis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M., Duchon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Duchon K.J., Evangelista C.C., Ferraz C., Ferraz C., Perriac S., Dunkov B.C., Dunn P., Duchon K.J., Evangelista C.C., Ferraz C., Ferraz C., Perriac S., Dunkov B.C., Dunkov B.C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Andrew D., Helman T.J., Harris M., Karpen S., Harris M., Karpen G.H., Ke Z., Guan P., Harris M., Katlush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalush F., Karpen G.H., Kez X., Kenison J., Moshrefi A., Mouston K., Mushand T.J., Wei M.-H., Ibeeyam C., Jaskov P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Muzny D.M., Mushon K., Moshrefi A., Moshrefi A., Mount S.M., Mohner R.D., Mount S.M., Mohner R.D., Mount S.M., Mohner R.D., Nowley M., Murphy B., Murphy L., Muzny D.M., Mushon K., Sanders R.D., Pollard J., Puzi Y., Rector G., Turner R.D., Wang A.H., Wang A.H., Wang X., Mullans S.M., Woodage T., Weinsenhaden J., Shipson M., Stupson M., Stupson M., Stupson M., Stupski M.P., Smith T., Shipson M., Who Stenber G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles G., Charles
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A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Coup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibeyam C., Jalai M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIncosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeteler R.,

Phouanenavong S., Pittman G.S., Patel S., Richards S., Scheler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergmann C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Shaburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Shunotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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FlyBase; Submitred (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AR003823; AAFS8560.2; '-.

SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 IDQYNNSSSLRN-----HLNNLEDIMAQISITNGDKE-----VEDYEKNIKKARNKL 111
                                                                                                                                                                                                                                                            7 DNVLNLEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHI- 65
                                                                                                                                                                                                                                                                                                        24 GOIQGIKDOYLBGKEYGY-----QTGFQRFLIIGYIQELMKFWLSH--------64
                                                                                                                                                                                    11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20277482; PubMed=10819331; Mirosawa M., Ohara O.; Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.; Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Chara O.; Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Chara O.; Prediction of the coding sequences of unidentified human genes.XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; NASA 9962; BAA96053.1; -. Hypothetical protein.
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NCBI_TaxID=139,
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 AQQQLKHIDKVRRSLEQLRSLIEEFPRINDPQADIVGAVQDIRSSHRRLR 115
                                                                                                                                                                                                                                                                                                                                                                                                                 66 -- DOYNNSSSLRNHLMNLEDIMAQISITNGDK-EVEDYEKNIKKARNKLR 112
                                                                                                                Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 1680;
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25.2%; Pred. No. 60;
tive 27; Mismatches 40; Indels
                                                                                                                                                                                    42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1680 AA; 194698 MW; BE3AF4E4E0013288 CRC64;
PlyBase; FBgn0033693; CG13175.
SEQUENCE 141 AA; 15724 MW; CA0016D1658BAC84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last amnotation update)
Hypothetical protein KIAA1529 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                            Query Match
Best Local Similarity 25.5%; Pred. No. 3.2;
Matches 28; Conservative 29; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 192 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conserved hypothetical protein.
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Best Local Similarity 25.2<sup>§</sup>
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Q9P1Z9
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Q9S062
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Query Match 11.9%; Score 91.5; DB 5; Length 5251; Best Local Similarity 23:0%; Pred. No. 4.2e+02; Matches 41; Conservative 35; Mismatches 39; Indels 63;
                                                                                                                                                                                                                                                                                                    Přil 0240.
Plasmodium falciparum (isolate 3D7).
Bukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE014839; AAN35824.1; -.
SEQUENCE 5251 AA; 617371 MW; 14C220359A132AD1 CRC64;
                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2002 (TrEMBLrel. 20, Created)
-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last amotation update)
Putative flagellar assembly protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AA
                                                                                                                                                                                                      PRT; 5251 AA
                                                                                  126 SLDNLVKEV-----GGTLQVSENPDDM 147
                                                                                                                 179 ILDTVKASVEALPIAGHAITLKLNPEDV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                     Dynein heavy chain, putative.
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                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 419:498-511(2002)
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=3D7;
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                                                                                                                                                                                                    Q8IID4
08IID4;
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                                                                                                                                                                 RESULT 13
Q8IID4
ID Q8IID
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                                                                                                                                                                                                                                                                                                                                                                                              64 KINN---VKNELNAKIDSVEKNLQKDISSLDIKIDSVEKNLQKDISSLNIKIDSVEKNLQ 120
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                                                                                                                                                                                                                                                                                                                                       10 NIGNIKNEFLEIGFSEEAIDFV---FLHNDNYNFE--FLKEKLINLEKNLOKD-ISNLDI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=E1 Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Pleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
           Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R., White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R., Palmer N., Haft D. P., Stevenson B., Stevenson B., Stevenson B., Stevenson B., A bacterial genome in flux: The twelve linear and nine circular extracthromosomal DNAs in an infectious isolate of the Lyme disease moli of microbial burgdorferi."; Microbial burgdorferi."; Microbial DNASON D. O. (1999).

InterPro, IPRO03900, KID.—Sepeat.
Pfam. PRO0354, KID., T.—Fepeat.
PHypothetical protein; Plasmid.
SEQUENCE 192 As, 22050 WW; B419C48522D0180E CRC64;
                                                                                                                                                                                                                                                                                                    8 NVLNLEBEGYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRPLIIGYIQELMKFWLSHID-
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11.9%; Score 92; DB 16; Length 270;
Best Local Similarity 22.3%; Pred. No. 13;
Matches 33; Conservative 31; Mismatches 42; Indels 42; Gaps
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                   54; Indels 15;
                                                                                                                                                                                                                                  12.2%; Score 94.5; DB 2; Length 192; 29.0%; Pred. No. 5.4; tive 29; Mismatches 54; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AA; 29994 MW; 4934AAEFB8939C4F CRC64;
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01-OcT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Flagellar assembly protein FliH, putative.
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Pfam; PF02108; FliH; 1.
PRINTS; PR01003; FLGFLIH.
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TIGR; VC2131; -.
                                                                                                                                                                                                                                                  Local Similarity 29.08
ses 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE FROM N.A.
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1587 DDDNIKNDKDEKDEKEETIIKLISSYGEEICNFHEGLV-----LKGKVECYLND---- 1635
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                                                                                        146 DILIN-----AQV----EKQLVD-------MVLALTKEVVHVEVQTNPQV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angluoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
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65 IDQYNNSSSLRNHLNNLEDIMAQIS--ITNGDKEVEDYEKNIKKARNKLRVIASITKETW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 IDQYNNSSSLRNHLNNLEDIMAQIS--ITNGDKEVEDYEKNIKKARNKLRVIASITKETW 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 ----GRIEGRQSELASFNDVIKPFSGYITQLHTYLETYEQ--RRRDELLQLVEKVTRQVI 139
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MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perra N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Promice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Slammonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DNVINLEBEQYEL - GFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSH
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.8%; Score 91; DB 16; Length 239;
Best Local Similarity 26.5%; Pred. No. 13;
Matches 41; Conservative 25; Mismatches 57; Indels 32; 'Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
VCBI_TaxID=632;
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                                                                                                                                                                                                          Nature 413:523-527(2001).

EMBL, AJ414144; CAC89567.1; -.

InterPro; IPR001563; Flag_FliH.

Pfam, PF02108; FliH; 1.

Flagella; Hypothetical protein; Complete proteome.

SEQUENCE 239 AA; 26725 MW; 6088795DBE257B09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genty http://www.nequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL, AE011949; AAM87011.1; -.
BYPOTHERICAL protein.
SEQUENCE 247 AA; 27690 MW; 666022F0B496D008 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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STRAIN=CO-92 / Biovar Orientalis;
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Matches 41; Conserv
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Search completed: February 16, 2004, 14:14:12 Job time : 35 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 16, 2004, 14:09:06; Search time 12 Seconds Run on:

(without alignments) 579.996 Million cell updates/sec

Title:

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	gaccharon	borrel												F19401 streptococc	~				P38929 saccharomyc		P08862 anabaena sp		P47025 saccharomyc	-		_		P16546 mus musculu		92	Q10947 caenorhabdi	56 B ac	91 8
	QI	YNOO YEAST	MUTL_BORBU	FLGK_BORBU	RASO_METUA		RASO_THEMA		RASO_PYRAB	TRP6_MOUSE	SMC1_YEAST	MYSB_CAEEL	K6PF SALTY	SYK BORBU	M12_STRPY	Y373 BOVIN	SPCA_HUMAN	RASO_AQUAE	DPOL_THEG8	ATC2_YEAST	YJ42_YEAST	XISA_ANASP	MEPB RAT	YJL2_YEAST	YBS6 METUA	SYI AQUAE		DYH9 HUMAN	SPCN_MOUSE		YAB1 YEAST			IF2P_SULAC
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RESULT 2

P31068 escherichia	Q8euw9 mycoplasma	P06998 escherichia	020159 chlorella v	P02468 mus musculu	P22194 schizosacch	P94523 bacillus su	P20192 sus scrofa	Q97wh0 sulfolobus	Q04747 bacillus su	051737 borrelia bu	Q97fk1 clostridium
FLIH ECOLI	GIDB MYCPE	K6P1_ECOLI	YCX7 CHLVU	LMG1 MOUSE	SD22_SCHPO	ARAA BACSU	KDGA_PIG	RASO_SULSO	SRF2_BACSU	MUTS_BORBU	SBCC_CLOAB
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1 Similarity 35.9%; Pred. No. 3.7e-11;
47; Conservative 30; Mismatches 40; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                            Hegemann J.H.; "Sequence analysis of the 33 kb long region between ORC5 and SUI1 from the left arm of chromosome XIV from Saccharomyces cerevisiae.";
                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungi; Aecomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 23.3 kba protein in ORC5-ATX1 intergenic region.
VNL260C OR NOB38.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
MEDLINE=97377992; PubMed=9234673;
Sen-Gupta M., Gueldener U., Beinhauer J.D., Fiedler T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 198 AA; 23328 MW; 2560D990E8A709F1 CRC64;
                 198 AA.
                 PRT;
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               STANDARD;
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145 -LITLHRLVKD 154
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P53846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 IGNIPSDNFLEFEEPPNKNEKEEIKFNYIGQI-------FSEFLIVEKI 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 NEIY-----FIDOHAVHEKIIYEKLRNSKKONVOKLLVPIEFTVVDKNIEEIIDSEIEEEYK 503
                                                                                                                                                                       MEDLINE=98665943; PubMed=9403685,
MEDLINE=98665943; PubMed=9403685,
MEDLINE=98665943; PubMed=9403685,
Lathigra R., White O., Kerdnum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer M., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fuji C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                      NATURE 390:580-586 (1997).

-I- FUNCTION: THIS PROTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN DNA. IT IS REQUIRED FOR DAM-DEPENDENT METHYL-DIRECTED DNA MISMATCH REPAIR. MAY ACT AS A "MOLECULAR MATCHAARRR", A PROTEIN THAT PROMOTES THE FORMATION OF A STABLE COMPLEX BETWENT TWO OR WORE DNA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF BEING PART OF A FINAL EFFECTOR COMPLEX (BY SIMILARITY: SELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSDIDIDNVLNLEE-----EQYELGFKE-GQIQGTKDQYLEGKEYGYQTGFQRFLIIGYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Gaps
                                                                                                  Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Match 12.6%; Score 97.5; DB 1; Length 610; Local Similarity 24.7%; Pred. No. 1.4; onservative 27; Mismatches 51; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00058; mutl; 1.
PROSITE; PS00058; DNA MISMATCH_REPAIR_1; 1.
DNA repair; Complete proteome.
SEQUENCE 610 AA; 71542 MW; 36A41A8A884EC9FA CRC64;
                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 NKLRVIASITKETWKIDSLDNLVKEVGGTL 138
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InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR002099; DNA mis_repair.
Pfam; PF01119; DNA mis_repair; 1.
Pfam; PF02118; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
                                                                  DNA mismatch repair protein mutL.
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HSSP; P23367; 1BKN.
TIGR; BB0211; -.
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SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=139;
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BORBU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no neadfiled and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
STRAIN=B8065943; Pubmed 4903685;
Fraser C.M., Casjens B., Hang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer M., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
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6D38B2F934900FF1 CRC64;
P70859, 051199, 051891, 051891, 051891, 051897 (Sel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2010 (Rel. 40, Last annotation update) 16-OCT-2010 (Rel. 40, Last annotation update) 16-OCT-2010 (Rel. 40, Last annotation update) 16-OCT-2011 hober associated protein 1 (HAP1). 17-OCT-2011 burgdorferi (Lyme disease spirochete) 18-OCT-2011 and 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (Lyme disease spirochete) 18-OCT-2011 (
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-!- SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ge Y., Old I.G., Saint-Girons I., Charon N.W.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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A -> R (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
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InterPro; IPR0012471; Flag bbookaP1.
PRINTS; PR01005; FRAGEMOKAP1.
PROSITE; PS00588; FLAGEMIA BB_ROD; FALSE_NEG.
Flagella; Complete proteome.
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EMBL; AE001129; AAC66579.1; -.
EMBL; AJ003222; CAA06002.1; -.
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43; Conservative
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                                         Best Local Similarity
Matches 43; Conserv
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Query Match
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RASO_THEMA
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-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RADSO SUBFAMILY.

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                                                                                                      173 IKITIDE------ANNYIRNIANIANIKQISKSQAMKDNPNDLMDARDLMVEKLGN 220
                                   ISITNGDKEVEDYEKNIKKARNKIRVIASITKETWK------IDSLDNLVKEVGG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IPR003499; -; 1.

R InterPro; IPR003499; ABC_transporter.

R InterPro; IPR003495; ABC_transporter.

R InterPro; IPR003495; SMC C.

InterPro; IPR003495; SMC N.

R Pfam; PF02483; SMC N; 1.

R Pfam; PF02483; SMC N; 1.

R Pfam; PF02483; SMC N; 1.

R Pfam; PF02483; SMC N; 1.

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R MART; SM00382; AAA; 1.

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R DM IND SMARY; SM00382; AAA; 1.

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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=6688087;
MEDLINE=96337999; PubMed=6688087;
Built C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Rerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Ratich C.I.,
Overbeek R., Kirkness E.W., Weidman J.F., Puhrmann J.L., Nguyen J.
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow F.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.W., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mre11 complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mre11 by unwinding and/or repositioning DNA ends into the mre11 active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
Archaea, Euryarchaeota, Methanococci, Methanococcales,
Methanocaldococcaceae, Methanocaldococcus.
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16-OCT-2001 (Rel. 40, Last sequence update)
18-EEB-2003 (Rel. 41, Last annotation update)
DNA double-strand break repair rad50 ATPase.
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                                                                                                                                                                                                                                                                                                                   221 IISVSIENKOD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                       137 TLQVS-ENPDD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A64465; A64465.
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                                                                                                                                                                                                                                 342 DIDNLDTLINKINDBIERVETIKDLLEELKNINBEIEKIEKYKRICEECKEY----YEK 396
                                                                                                                                                                                                                                                                                                                                                                                                                 397 YLELEEKAVEYNKLTLEYITLLQEKKSIEKNINDLETRINKLLEETKNIDIESIENSLKE 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 QELMKFWLSHIDQYNNSSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKAR-NKLRV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DID-IDNVLN-------LEEEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQR 47
                                                                                                                                                                                                                                                                                                                                    ----SITNGDKE 96
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                                                                                 62; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 87; DB 1; Length 1539;
20.8%; Pred. No. 27;
tive 36; Mismatches 64; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 VEDYEK---NIKKARNKL-RVIASITKETWKIDSLDNLVKEVGGTLQVSENPDD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97349984; PubMed=9205841;
Magase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tankawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tankawa K.-I., Kotani H., Nomura N., Ohaca O.,
"Prediction of the coding sequences of unidentified human genes. VI
"Prediction of the coding sequences of unidentified human genes. VI
"The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 4:141-150(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
11.9%; Score 91.5; DB 1; Length 1005; 24.7%; Pred. No. 7.3; trive 34; Mismatches 62; Indels 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1539 AA; 180065 MW; D901314E981BF001 CRC64;
                                                                                                                                                                                                                                                                                                                                    48 FL-IIGYIQELMKFWLSHIDQYNNSSSLRNHLNNLEDIMAQI----
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Hypothetical protein; Coiled coil.

COILED COIL (POTENTIAL)

1514
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16-OCT-2001 (Rel. 40, Last sequence update) /
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 IASITKETWKIDSLDNLVKEVGGTLQVSE 142
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Pyrococcus horikoshii,
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                                                                                                                               SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=53953;
                                            RAD50 OR PH0929.
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                                                                                                                                                                              70 NSSSLRNHLNNLEDIMAQISITNGDKEVEDYEKNIKKARNKLRVI-----ASITKET 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 NLKSIRNQIEKIBEELHRLGYS-----EDLEEKLDEKRKKLRKIEBERHSISQKITAAD 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 NLEBEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQ-YN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.9%; Score 84.5; DB 1; Length 852;
Best Local Similarity 21.2%; Pred. No. 22;
Matches 32; Conservative 35; Mismatches 49; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; D),z25; -.
TIGA; TMG536; -.
TIGA; TMG6349; -; 1.
ThAMAP, MF 00449; -; 1.
FRAM; PP02463; SMC_N, 1.
PFAM; PP02463; SMC_N, 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
NP_BIND 30 37 ATP (BY SIMILARITY).
155 711 COILED COIL. (POTENTIAL).
155 711 COILED COIL. (POTENTIAL).
156 711 TOTOL (MY, 31BA9F72A4EC5CD2 CRC64;
                                                                                                   Thermotoga maritima.
Sacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Forms a complex with mrell (By similarity).
-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RADSO SUBFAMILY.
                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable DNA double-strand break repair rad50 ATPase.
RAD50 OR TM1636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 WKIDSLDNLVKEVGGTLQ----VSENPDDM 147
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ID RASO_PYRHO STANDARD;

C OS8687;

DT 16-OCT-2001 (Rel. 40, Created)
 STANDARD;
                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
                                                                                                                             NCBI_TaxID=2336;
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                                                                                                                  Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 ELSEIEDRLLRLGFKTIDELSGRIRELEKFHNKYIBAKNAEKELRDILESLKDEREELDK 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------SITNGDKEVE---DYEKNIKKARNKLRVIASITKETWKIDSLDNLVK 132
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R InterPro; IPR003593; AAA_ATPase.

R InterPro; IPR003495; SMC_Transporter.

R InterPro; IPR003495; SMC_N.

InterPro; IPR003495; SMC_N.

R Pfam; PF02463; SMC_N.

R Pfam; PF02463; SMC_N; 1.

R Pfam; PF02463; SMC_N; 1.

R R Pfam; PF02463; SMC_N; 1.

R Pfam; PF02463; SMC_N; 1.

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R Pfam; Pf02463; SMC_N; 1.

R Pfam; Pf02463; SMC_N; 1.

R Pfam; Pf
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-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA double-strand break repair rad50 ATPase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 ---ITNGDKEVEDYEKNIKKARNKL--------RVIASITKETWKIDSLDNL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 NLE----ELEQKEREFEGINEEFNKIKGELIGLERDLKRIKALEGRRKLIEBKVRKAKEE 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 NLEEEQYELGFKEGQIQGTKDQY--LEGKEYGYQTGFQRF-----LI----- 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 -----IGY-----IQELMKFWLSHIDQYNNSSLRNHLMNLEDIMAQIS-- 89
                                                                                                                                                                                                                                                                                                Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch G.N., Barbe V., Plament D., Galperin M., Heilig R., Lecompte O., Poch O., Y., Weisenbach J., Zivanovic Y., Forterre P.;
"An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococus abyss: ",
Mol. Microbiol. 47:1495-1512(2003).
"Involved in DNA double-strand break repair (DSBR). The redSO/merll complex possesses single-strand endounclease activity and ATP-dependent double-strand-specific exonuclease activity.
Rad50 provides an ATP-dependent control of meell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Mismatches 49; Indels 67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIRMAP; MF 00449; -: 1.

InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003395; ABC_transporter.
InterPro; IPR003395; MC_N.
Pfam; PF04423; Rad50_zn_Eook; 1.
ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
NP BIND 30 37 ATP (BY SIMILARITY).
SEQUENCE 880 AA; 103970 MW; FPB177EC7E026479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%; Score 83.5; DB 1; Length 880; 20.1%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Forms a complex with mrell (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. RADSO SUBFAMILY.
                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
DNA double-strand break repair rad50 ATPase.
RAD50 OR PYRAB12200 OR PAB0812.
    880 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ248286; CAB50131.1; -.
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; F75103; F75103.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-GES / Orsay;
PubMed=12622808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                        NCBI_TaxID=29292;
                                                                                                                                        Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity
  PYRAB
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RASO PYR
O9UZČ8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRP6 MOUSE STANDARD; PRT; 930 AA. 091143; 092211; 09211; 09211; 092211; 092211; 092211; 092211; 092211; 092211; 092211; 09222000 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Short transient receptor potential channel 6 (TrpC6) (Calcium entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Ltp, a novel mammalian gene family essential for agonist-activated capacitative Ca2+ entry.";
Cell 85:661-671(1996).
                                                                                                                                                                                                                                                                                    "Cloning and expression of a novel mammalian homolog of Drosophila transient receptor potential (Trp) involved in calcium entry second to activation of receptors coupled by the Gq class of G protein."; J. Biol. Chem. 272:29672-29680(1997).
                                                                                                                                                                                                                                                                                                                                                                                                            Buess M., Engler O., Hirsch H.H., Moroni C.;
"Search for oncogenic regulators in an autocrine tumor model using
differential display PCR: identification of novel candidate genes
including the calcium feanuel mtrp6.";
Oncogene 18:1487-1494 (1999).
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
                                                                                                                                                                                                                                                       Boulay G., Zhu X., Peyton M., Jiang M., Hurst R., Stefani E.
Birnbaumer L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 3 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99158172; PubMed=10050885;
                                                                                                                                                                                                                                       MEDLINE=98037793; PubMed=9368034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Brain;
MEDLINE=96234226; PubMed=8646775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 631-739 FROM N.A.
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                                                                                                     IRPC6 OR TRRP6 OR TRP6.
                                                                                                                            (Mouse)
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                            Mus musculus
                                                                                                 channel
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EMBL, AF057749; AAC64394.1; -. MGD; MGI:109523; Trpc6. GO; GO:0015279; F:store-operated calcium channel activity; IDA.

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   P:cytosolic calcium ion concentration elevation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 29;
29; Mismatches 49; Indels 31; Gaps
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01-0CT-1993 (Rel. 27, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Structural maintenance of chromosome 1 (DA-box protein SMC1).
SMC1 OR CHL10 OR YFL008W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetine; Saccharomycetales; Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                            SWART; SM00248; ANK; 2.
TIGREPAMS; TIGRO0870; trp; 1.
PROSITE; PS50289; ANK REPEAT; 1.
PROSITE; PS50297; ANK REP REGION; 1.
Ionic channel; Transmembrane; Ion transport; Calcium channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 83.5; DB 1; Length 930;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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MISSING (IN REF. 2).
V -> A (IN REF. 2).
V -> B (IN REF. 2).
N -> D (IN REF. 2).
S -> A (IN REF. 2).
D -> Y (IN REF. 2).
D -> Y (IN REF. 2).
S -> T (IN REF. 2).
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                             InterPro; IPR002110; ANK.
InterPro; IPR002110; ANK.
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR002153; Trans_receptor.
InterPro; IPR004729; Trp_CaChannel.
InterPro; IPR004662; TRPChannele.
Pfam; PF00023; ank; 4.
Pfam; PF00023; ank; 4.
PRINTS; PR01697; TRNSRECEPTRP.
PRINTS; PR01697; TRNSRECEPTRP.
PRINTS; PR01697; TRNSRECEPTRP.
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ses 37; Conserv
   GO; GO:0007204;
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P32908;
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DNA replication. The cohesion during cell cycle and in DNA replication. The component of cohesion complex. The cohesion of sister chromatide after DNA replication. The cohesion of sister chromatide after complex is required for the cohesion of sister chromatide after chromatide rather complex is cleaved and dissociates from complex is cleaved and dissociates from chromatin, allowing sister chromatide to segregate.

Chromatin, allowing sister chromatide to segregate.

CHERNITY: Cohesin complexes are composed of the SMCI and SMCI heterodimer attached via their hinge domain, MCDI/SCCI which link them, and IRRI/SCC3, which interacts with MCDI. The cohesin complex also interacts with SCC2, which is required for its association with chromosome with SCC2, which is required for its association with chromosome arms. At anaphase, the MCDI scattered along chromosome arms. At anaphase, the MCDI subunit of the cohesin complex is cleaved, allowing chromosome separation.

Leading to the dissociation of the complex from chromosomes, allowing chromosome separation.

Leading to the dissociation of the complex from chromosomes, allowing chromosome separation.

CHERNITY THE FLEXIBLE Hinge domain, which separates the large interaction with the corresponding of SMC3, forming a vename tech by different ends of the cleavable MCDI protein, forming a ring structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=9990856;
Toth A., Ciosk R., Uhlmann F., Galova M., Schleiffer A., Nasmyth K.;
"Yeast cohesin complex requires a conserved protein, Ecolp(Ctf7), to establish cohesion between sister chromatids during DNA replication.";
                                         SEQUENCE FROM N.A., AND MUTANTS SMC1-1 AND SMC1-2.
MEDLINE=94103320; PubMed=8276886;
Strunnikov A.V., Larionov V.L., Koshland D.;
Skrunnikov A.V., Larionov Y.L., Koshland D.;
SMC1: an essential yeast gene encoding a putative head-rod-tail protein is required for nuclear division and defines a new ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION IN A COHESIN COMPLEX WITH SMC3; IRR1 AND MCD1, AND INTERACTION OF THE COHESIN COMPLEX WITH SCC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DENTIFICATION IN A COHESIN COMPLEX WITH SMC3; MCD1 AND IRR1, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haering C.H., Loewe J., Hochwagen A., Nasmyth K., "Molecular architecture of SMC proteins and the yeast cohesin
                                                                                                                                                                                                                                               STRAIN=S288C / AB972;
MEDLINE=95400292; PubMed=7670463;
Muradami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the SMC family. SMC1 subfamily.
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GO; GO:0008278; C:cohesin complex; IDA
                                                                                                                                                            tein family.";
Cell Biol. 123:1635-1648(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 10:261-268(1995).
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EMBL; D50617; BAA09230.1; -.
PIR; A49464; A49464.
SGD; S0001886; SMC1.
                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae."
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex.";
Mol. Cell
                                                                                                                                                               protein
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61 WLSHIDQYNNSSSLRNHINNLEDIMAQISITNGDKE--VEDYE-----KNIKKAR 108
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                                                                                                                                                                                                                                               COILED COIL (POTENTIAL).
PLEXIBLE HINGE.
COLLED COIL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ALA/ABS-RICH (DA. BOX).
S.-L: IN TS MUTANT SMC1-2.
N.-D: IN TS MUTANT SMC1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s; Pred. No. 48;
36; Mismatches 50; Indels 39; Gaps
                                                                                                                                                              ; SMC C; 1.
cycle; Chromosome partition; ATP-binding; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 850-1966 FROM N.A.
MEDLINE=82272395, PubMed=7202124;
McLachlan A.D., Karn J.;
"Periodic charge distributions in the myosin rod amino acid sequence match cross-bridge spacings in muscle.";
Nature 299:226-231(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
GO; GO:0003680; F:AT DNA binding activity; IDA.
GO; GO:0000217; F:DNA secondary structure binding activity; IDA.
GO; GO:000369; F:Gouble-stranded DNA binding activity; IDA.
GO; GO:0000070; P:mitchic chromosome segregation; IMP.
InterPro; IPRO03405; SMC_C.
InterPro; IPRO03595; SMC_N.
Pfam; PF02463; SMC_V.
Pfam; PF02483; SMC_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-83273600; PubMed-6576334;
Karn J., Brenner S., Barnett L.;
Karny J., Brenner S., Gomains in the Caenorhabditis elegans unc-54
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
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MEDLINE-83232892; PubMed-6571695;
Wills Wills N. G.H.; Watern J., Barnett L., Bolten S.,
Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                           141279 MW; B504017AA0ECCA8C CRC64;
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21-UUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain B (MHC B).
                                                                                                                                                                                                                               ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Conservative
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489
678
1063
1164
173
458
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1129 116
173 17
458 45
1225 AA;
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Nuclear protein.
NP BIND 33
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MUTAGEN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DNVLNLEEEQYELGFKEGQIQGTKDQYLE-----GKEYGYQTGFQRFLIIGYIQELM 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --AQISIT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1080 ESGRQRHDLENNLKKKESELHSVSSRLEDEQALVSKLQRQIKD--GQSRISELEEL 1134
              HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

SUBCELLULAR LOCATION: TALL SEQUENCE of the wyofibrils.

SUBCELLULAR LOCATION: TALL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 FESTIDUS REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

FTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLAYTED AND ARE REQUIRED FOR MYOSIN ATHES SIDOMAIN ARE SELECTIVELY MISCELLANGOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY WEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 NGDKEVEDYEKNIKKARNKLRVIAS-ITKETWKIDSLDNLVKEVGGTLQVSENPDDM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Mismatches 59; Indels 46; Gaps
                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.
-!- SIMILARITY: Contains 1 myosin-like globular head domain.
  SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Multigene family.

DOMAIN
1 850 MYOSIN HEAD-LIKE.

DOMAIN 851 1966 COILE (POTENTAL).

DOMAIN 851 1164 ALPHA-HELICAL TAILPIECE ($2).
                                                                                                                                                                                                                                                  MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%; Score 82; DB 1; Length 1966; 20.9%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 E -> R (IN REF. 2).
80 I -> L (IN REF. 2).
225125 MW, B66F0BB2FE27B67F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HINGE.
LIGHT MEROMYOSIN (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (BY SIMILARITY)
ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 KFWLSHIDQYNN----SSSLRNHLNNLEDIM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004009; myosin head.
InterPro; IPR004009; Myosin N.
InterPro; IPR004009; Myosin N.
InterPro; IPR002408; Myosin Lail.
Pfam; PF00063; myosin head; 1.
Pfam; PF00736; Myosin N; 1.
Pfam; PR01576; Myosin Lail; 1.
Propom; PR00193; MYOSINHEAVY.
Probom; PR000355; mYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J01050; AAA28124.1; -.
EMBL; V01494; CAA24738.1; -.
HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1880
                                                                                                                                                                                                                               (82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   769 78
128 12
705 70
715 71
1337 133
1880 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                 SUBFRAGMENT
                                                                                                                                                                                                                                                                       C. ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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DOMAIN
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MOD RES
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashama D., Brooks K., Chillingworth T., Commerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Barrell B.G.; Barrell B.G.; Barrell B.G.; Multiple drug resistant Salmonella enterica servorar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
SPECUESS LYPH): STRAIN=TY2 / ATCC 700931;
SPECUESS LYPH): STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=15644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                               McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrellle P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 185:2330-2337(2003).

-1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1.6-bisphosphate.

-1- PATHWAY: Key control step of glycolysis.

-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-1- SIMILARITY: Belongs to the phosphofructckinase family.
                                                                                                                                                                                                                                                                                                                                         SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720, MEDLINE=21534948; PubMed=11677609;
                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                         320 AA.
                                                                                                                                                            (Phosphohexokinase)
PFKA OS STM4062 OR STX3809 OR T3557.
Salmonella typhimurium, and
Salmonella typhi.
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 00339; -; 1.
InterPro; IPR000023; Ppfruckinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE008889; AAL22902.1; -.
EMBL; AL627279; CAD09562.1; -.
EMBL; AE016846; AA071062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00365; PFK; 1.
PRINTS; PR00476; PHFRCTKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG?????; pfkA.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                        OBXG19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               StyGene;
RESULT 12
KGPF SALTY
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                                                                                                                                                                                                                                                                                                                          162 QRISIVEVMGRYCGDLTLAAAIAGGCEFIVVPEVEFUREDLVAEİKAGIAKGKKHAİVAI 221
                                                                                                                                                                                               18 ELGPKEGGIQGTKDQYLEGKEY--GYQTGFQRFLIIGYIQELMKFWLSHIDQYNNSSSLR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAID=98065943; PubMed=9403695;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Pererson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad, Sci. U.S.A. 97:14224-14228(2000).
-!- CATALYTIC ACTIVITY: ATP + L-1ysine + tRNA(Lys) = AMP + diphosphate
-!- L-1ysyl-tRNA(Lys).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MISCELLANEGUS: Able to charge E.coli tRNA(Lys) in vitro.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                          34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ibba M., Bono J.L., Rosa P.A., Soell D.;
"Archaeal-type lysyl-tRNA synthetase in the Lyme disease spirochete
Borrelia burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrella burgdorferi (Lyme disease spirochete),
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Lysyl-FRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
LYSS OR BB0659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20570460; PubMed=11121028; Soell D., Becker H.D., Plateau P., Blanquet S., Ibba M.; "Context-dependent anticodon recognition by class I lysyl-tRNA
                                                                                                            Query Match 10.5%; Score 81; DB 1; Length 320; Best Local Similarity 25.2%; Pred. No. 14; Matches 35; Conservative 23; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic seguence of a Lyme disease spirochaete, Borrelia
ProDom; PD000707; Ppfruckinase; 1.
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Kinase; Transferase; Glycolysis; Complete proteome.
SEQUENCE 320 AA; 34915 MW; 68BODDFCF689F420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 94:14383-14388(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       521 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98070760; PubMed=9405621;
                                                                                                                                                                                                                                                                                                                                                                                                               222 TEHMCDVDELAHFIEKETG 240
                                                                                                                                                                                                                                                                                                                                                                   118 TKETWKIDSLDNLV-KEVG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 KEEKKRAFK--RIYELSQPYMPSKRIPYQVGFRHLSVISQIFE-------NNINK 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 ILNYLKNVQEDQKDKLINKINCAINWIRDFAPEDFKFSLRSKFDNMEILEENSKKAINEL 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 EEQYELGFKEGQIQGTKDQYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQYNNSSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences.";
J. Bacteriol. 169:5633-5640(1987).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE DIFFERENT ANTIGENIC SEROTYPES
-!- FUNCTION: THIS PROTEIN M IS CLOSELY ASSOCIATED WITH VIRULENCE OF
THE BACTERIUM AND CAN RENDER THE ORGANISM RESISTANT TO
                                                                                                                                                                                                                                   HAMAP, MF_00177; -; 1.
Interbro; IPR002904; Lys tRNA-synt_lc.
Interbro; IPR0041412; tRNA-synt_l.
Interbro; IPR001412; tRNA-synt_l.
Interpro; IPR001412; tRNA-synt_lif; 1.
IIGRFAMA; ITGR00467; LysG_arch; 1.
PROSTIE; PS00178; AA TRNA_LIGASE 1; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRNIN=CG24 / Serotype M12;
MEDLINE=8808777; PubMed=2445730;
Robbins J.C., Spanier J.G., Jones S.J., Simpson W.J., Cleary P.P.;
"Streptococcus pyogenes type 12 M protein gene regulation by upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHAGOCYTOSIS.
SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 81; DB 1; Length 521; 21.5%; Pred. No. 24; tive 22; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 AA; 60938 MW; 6AF5A461AED3251D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "HIGH" REGION.
"KMSKS" REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M protein, serotype 12 precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 ------RVIASITKETWKIDSLDNL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 LDFLKKNFEVATEQDÍQNÉIYKÍSRENNI 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an amide bond (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                    EMBL, AECO1167, AAC67006.1; -- PIR; B70182; B70182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 21.59
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M12 STRPY
P19401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AYNELSGEAH----KDALGKLGIDNADLKAKITELEKSVEEKNDVLSQIKKELEEAEKDI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 EKQRLEDLGQKFERLKQRSELYLQQYYDNKSNGYKGDW-----YVQQL-KMLNRDLEQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 YNNSSSLRNHLNNLEDIMAQISITNGD-------KEVEDYEXNI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 BEEQYE-LGPKEGQIQGTKD----QYLEGKEYGYQTGFQRFLIIGYIQELMKFWLSHIDQ 67
                     R PIR; A40174; A60115.
R InterPro; PR00597; Gpos YSIRK.
R InterPro; IPR001899; Gram_Dos_anchor.
R InterPro; IPR001899; Gram_Dos_anchor.
R InterPro; IPR00346; Gram_Dos_anchor; I.R
R Pfan; PP00746; Gram_Dos_anchor; I.R
R PRINTS; PR001015; GP05ANGHOR.
R PRINTS; PR001168; YSIRK signal; I.R
R PROSITE; PS0844; Gram_Pos_ANGHOR.
R PROSITE; PS0844; Gram_Pos_ANGHOR.
W Virulence; Pragocytosis; Cell wall; Peptidoglycan-anchor; Repeat; Annay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Mismatches 48; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      M PROTEIN, SEROTYPE 12.
REMOVED BY SORTAGE (POTENTIAL).
COLLED COLL (POTENTIAL).
GLY/FRO-RICH (CELL WALL-SPANNING).
LPXTG SORTING SIGNAL (POTENTIAL).
AMIDE-LINKED TO CELL WALL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Wakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5%; Score 81; DB 1; Length 564; 22.6%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Trachea;
Jovov B., Ripoll P.J., Benos D.J.;
Submitted (AUG-1999) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN 37 1426 COLLED COLL (POTENTIAL).
SEQUENCE 1453 AA; 169934 MW; 03CBA02A64CF4139 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 546 LPXTG SORTING SIGNAL (FULE 545 AMIDB-LINKED TO CELL WALL 564 564 564 AA, 62904 MM; 5F1549DACAA77B46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 KKARNKLRVIASITKETWKIDSLDNLVKEVGGTLQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Coiled coil. DOMAIN 37 1426 COLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF176816; AAF00990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein KIAA0373
EMBL; M18269; AAA88573.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
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SEQUENCE
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DOMAIN
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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